

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

protein - protein search, using sw model  
on: December 16, 2003, 15:36:20 ; Search time 14.5792 Seconds  
(without alignments)  
266.996 Million cell updates/sec

le: US-09-920-137A-7  
fect score: 486  
quence: 1 MKLCVTVLSLLMLVAFCSP.....VCADPSESVMQYVYDLELN 92  
ring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
rched: 328717 seqs, 42310858 residues

al number of hits satisfying chosen parameters: 328717

imum DB seq length: 0  
imum DB seq length: 2000000000

it-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

abase : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

ult No.	Score	Query Match	Length	DB ID	Description
1	486	100.0	92	1	US-08-347-492B-11
2	486	100.0	92	1	US-08-375-346A-4
3	486	100.0	92	2	US-08-421-144A-4
4	486	100.0	92	2	US-08-798-143-11
5	486	100.0	92	2	US-08-467-123B-4
6	486	100.0	92	3	US-08-808-720-10
7	486	100.0	92	3	US-09-133-521-6
8	486	100.0	92	4	US-08-679-493A-157
9	486	100.0	92	4	US-08-679-493A-158
10	486	100.0	92	4	US-09-230-371A-24
11	486	100.0	331	3	US-08-808-720-7
12	482	99.2	92	3	US-09-230-637-41
13	482	99.2	92	4	US-08-679-493A-159
14	476	97.9	92	1	US-07-792-988-2
15	461	94.9	92	4	US-08-649-006A-9
16	461	94.9	92	4	US-09-771-023-11
17	457	94.0	92	4	US-08-480-449-22
18	448.5	92.3	91	1	US-08-679-493A-160
19	448.5	92.3	91	2	US-08-660-542-22
20	448.5	92.3	91	4	US-08-479-603-22
21	448.5	92.3	91	4	US-08-939-107-22
22	394	81.1	92	4	US-09-195-106-3
23	375	77.2	69	3	US-07-982-759F-35
24	375	77.2	74	2	US-08-450-905B-35
25	371	76.3	68	2	US-08-615-232A-10
26	371	76.3	68	3	US-08-470-323-10
27	359	73.9	69	2	US-08-716-188-6

28	353	72.6	65	1	US-08-330-163-15	Sequence 15, Appl
29	353	72.6	65	1	US-08-482-111-15	Sequence 15, Appl
30	320	65.8	93	1	US-08-230-574-4	Sequence 4, Appli
31	320	65.8	93	2	US-08-479-126B-6	Sequence 6, Appli
32	320	65.8	93	2	US-08-726-830A-6	Sequence 6, Appli
33	320	65.8	93	2	US-08-535-116-2	Sequence 2, Appli
34	320	65.8	93	3	US-09-044-855A-6	Sequence 6, Appli
35	320	65.8	93	3	US-09-044-855A-6	Sequence 6, Appli
36	320	65.8	93	3	US-09-230-637-39	Sequence 39, Appl
37	320	65.8	93	4	US-09-437-602-3	Sequence 3, Appli
38	320	65.8	93	4	US-09-151-450-2	Sequence 2, Appli
39	313	64.4	93	4	US-09-230-371A-23	Sequence 23, Appl
40	310	63.8	93	5	PCT-US96-10087-6	Sequence 6, Appli
41	303	62.3	80	1	US-08-173-209A-5	Sequence 5, Appli
42	300.5	61.8	92	1	US-07-792-988-1	Sequence 1, Appli
43	300.5	61.8	92	1	US-08-347-492B-10	Sequence 10, Appl
44	300.5	61.8	92	1	US-08-375-346A-3	Sequence 3, Appli
45	300.5	61.8	92	1	US-08-230-574-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1  
US-08-347-492B-11  
; Sequence 11, Application US/08347492B  
; Patent No. 5602008  
; GENERAL INFORMATION:  
; APPLICANT: Wilde, Craig G.  
; APPLICANT: Hawkins, Phillip R.  
; APPLICANT: Bandman, Olga  
; APPLICANT: Seilhamer, Jeffrey J.  
; TITLE OF INVENTION: EXPRESSED CHEMOKINES, THEIR  
; TITLE OF INVENTION: PRODUCTION AND USES  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: U.S.  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/347,492B  
; FILING DATE: 29-NOV-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/303,241  
; FILING DATE: 07-SEP-1994  
; APPLICATION NUMBER: 08/320,011  
; FILING DATE: 05-OCT-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Luther, Barbara J  
; REGISTRATION NUMBER: 33,954  
; REFERENCE/DOCKET NUMBER: PF-0024  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-852-0195  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 92 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; IMMEDIATE SOURCE:  
; LIBRARY: GENBANK  
; CLONE: GI 127080  
US-08-347-492B-11

Query Match 100.0%; Score 486; DB 1; Length 92;  
Best Local Similarity 100.0%; Pred. No. 1.3e-50;  
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKLCVTVLSLLMLVAAFCSPPALSGSDPTACCFSTARKLPNRFVVDYETSSLCSSQ 60  
|||||  
1 MKLCVTVLSLLMLVAAFCSPPALSGSDPTACCFSTARKLPNRFVVDYETSSLCSSQ 60

61 PAVVFQTKRSKQVCADPSESWSVQYVVDLELN 92  
|||||

61 PAVVFQTKRSKQVCADPSESWSVQYVVDLELN 92  
|||||

SULT 2

-08-375-346A-4  
Sequence 4, Application US/08375346A  
Patent No. 5605817  
GENERAL INFORMATION:

APPLICANT: Coleman, Roger  
APPLICANT: Wilde, Craig G.  
APPLICANT: Seilhamer, Jeffrey J.  
TITLE OF INVENTION: A NEW CHEMOKINE EXPRESSED IN FETAL SPLEEN,  
TITLE OF INVENTION: ITS PRODUCTION AND USES  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:

ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3330 HILLVIEW AVENUE  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSEQ Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/375,346A  
FILING DATE: 19-JAN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: LUTHER, BARBARA J.  
REGISTRATION NUMBER: 33,954  
REFERENCE/DOCKET NUMBER: PF-0026 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 855-0555  
TELEFAX: (415) 855-0572  
TELEX:

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 92 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal

ORIGINAL SOURCE:

-08-375-346A-4

Query Match 100.0%; Score 486; DB 1; Length 92;  
Best Local Similarity 100.0%; Pred. No. 1.3e-50;  
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKLCVTVLSLLMLVAAFCSPPALSGSDPTACCFSTARKLPNRFVVDYETSSLCSSQ 60  
|||||  
1 MKLCVTVLSLLMLVAAFCSPPALSGSDPTACCFSTARKLPNRFVVDYETSSLCSSQ 60

QY 61 PAVVFQTKRSKQVCADPSESWSVQYVVDLELN 92  
|||||  
Db 61 PAVVFQTKRSKQVCADPSESWSVQYVVDLELN 92  
|||||

RESULT 3

US-08-421-144A-4  
Sequence 4, Application US/08421144A  
Patent No. 5874211  
GENERAL INFORMATION:

APPLICANT: BANDMAN, OLGA  
APPLICANT: COLEMAN, ROGER  
APPLICANT: STUART, SUSAN G.  
TITLE OF INVENTION: NEW CHEMOKINE EXPRESSED IN EOSINOPHILS  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:

ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/421,144A  
FILING DATE: 13-APR-1995  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Luther, Barbara J.  
REGISTRATION NUMBER: 33954  
REFERENCE/DOCKET NUMBER: PF-0031 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-852-0195

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:  
LENGTH: 92 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-421-144A-4

Query Match 100.0%; Score 486; DB 2; Length 92;  
Best Local Similarity 100.0%; Pred. No. 1.3e-50;  
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLCVTVLSLLMLVAAFCSPPALSGSDPTACCFSTARKLPNRFVVDYETSSLCSSQ 60  
|||||  
Db 1 MKLCVTVLSLLMLVAAFCSPPALSGSDPTACCFSTARKLPNRFVVDYETSSLCSSQ 60  
|||||

QY 61 PAVVFQTKRSKQVCADPSESWSVQYVVDLELN 92  
|||||

Db 61 PAVVFQTKRSKQVCADPSESWSVQYVVDLELN 92  
|||||

RESULT 4

US-08-798-143-11  
Sequence 11, Application US/08798143  
Patent No. 5936068  
GENERAL INFORMATION:

APPLICANT: Wilde, Craig G.  
APPLICANT: Hawkins, Phillip R.  
APPLICANT: Bandman, Olga  
APPLICANT: Seilhamer, Jeffrey J.  
TITLE OF INVENTION: EXPRESSED CHEMOKINES, THEIR  
TITLE OF INVENTION: PRODUCTION AND USES  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/798,143  
FILING DATE: 10-FEB-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/347,492  
FILING DATE: 29-NOV-1994  
APPLICATION NUMBER: 08/303,241  
FILING DATE: 07-SEP-1994  
APPLICATION NUMBER: 08/320,011  
FILING DATE: 05-OCT-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Luther, Barbara J  
REGISTRATION NUMBER: 33,954  
REFERENCE/DOCKET NUMBER: PF-0024  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-852-0195  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 92 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
LIBRARY: GENBANK  
CLONE: GI 127080  
-08-798-143-11

Query Match 100.0%; Score 486; DB 2; Length 92;  
Best Local Similarity 100.0%; Pred. No. 1.3e-50;  
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 MKLCVTVLSLLMLVAAPSPALSGDPPTACCFSTARKLPNRFVVDYETSSLC SQ 60  
|||||  
1 MKLCVTVLSLLMLVAAPSPALSGDPPTACCFSTARKLPNRFVVDYETSSLC SQ 60  
61 PAVVFQTKRSKQVCADPSESWSVQYVVDLELN 92  
61 PAVVFQTKRSKQVCADPSESWSVQYVVDLELN 92

SULT 5  
-08-467-123B-4  
Sequence 4, Application US/08467123B  
Patent No. 5945506  
GENERAL INFORMATION:  
APPLICANT: Coleman, Roger  
APPLICANT: Wilde, Craig C.  
APPLICANT: Seilhamer, Jeffrey J.  
TITLE OF INVENTION: CHEMOKINE EXPRESSED IN FETAL SPLEEN,  
TITLE OF INVENTION: ITS PRODUCTION AND USES  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,123B  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/375,346  
FILING DATE: 19-JAN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0026-1 DIV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-555-0555  
TELEFAX: 415-845-4166  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 92 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-467-123B-4  
Query Match 100.0%; Score 486; DB 2; Length 92;  
Best Local Similarity 100.0%; Pred. No. 1.3e-50;  
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLCVTVLSLLMLVAAPSPALSGDPPTACCFSTARKLPNRFVVDYETSSLC SQ 60  
|||||  
Db 1 MKLCVTVLSLLMLVAAPSPALSGDPPTACCFSTARKLPNRFVVDYETSSLC SQ 60  
QY 61 PAVVFQTKRSKQVCADPSESWSVQYVVDLELN 92  
Db 61 PAVVFQTKRSKQVCADPSESWSVQYVVDLELN 92

RESULT 6  
US-08-808-720-10  
Sequence 10, Application US/08808720  
Patent No. 6100387  
GENERAL INFORMATION:  
APPLICANT: Herrmann, Steve  
APPLICANT: Swanberg, Stephen  
TITLE OF INVENTION: CHIMERIC POLYPEPTIDES CONTAINING  
TITLE OF INVENTION: CHEMOKINE DOMAINS  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genetics Institute, Inc.  
STREET: 87 CambridgePark  
CITY: Cambridge  
STATE: MA  
COUNTRY: USA  
ZIP: 02140  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/808,720  
FILING DATE:  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Sprunger, Suzanne  
REGISTRATION NUMBER: P-41,323  
REFERENCE/DOCKET NUMBER: GI5291  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 498-8284  
TELEFAX: (617) 876-5851

## INFORMATION FOR SEQ ID NO: 10:

## SEQUENCE CHARACTERISTICS:

LENGTH: 92 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

3-08-808-720-10

Query Match 100.0%; Score 486; DB 3; Length 92;

Best Local Similarity 100.0%; Pred. No. 1.3e-50;

Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

/ 1 MKLCVTVLSLLMLVAAFCSPALSAPMGSDPPTACCFSTYARKLPRNFVVDYYETSSLCSQ 60

/ 1 MKLCVTVLSLLMLVAAFCSPALSAPMGSDPPTACCFSTYARKLPRNFVVDYYETSSLCSQ 60

/ 61 PAVVFQTKRSKQVCADPSESWSVQYVYDLELN 92

/ 61 PAVVFQTKRSKQVCADPSESWSVQYVYDLELN 92

## RESULT 7

3-09-133-521-6

Sequence 6, Application US/09133521

Patent No. 6281200

GENERAL INFORMATION:

APPLICANT: Fife, Kenneth H.

APPLICANT: Krathwohl, Mitchell D.

APPLICANT: Brown, Robert

APPLICANT: Brown, Darron R.

APPLICANT: Broxmeyer, Hal E.

TITLE OF INVENTION: FUNCTIONAL CHARACTERIZATION OF THE C-C CHEMOKINE-LIKE

TITLE OF INVENTION: MOLECULES ENCODED BY MOLLUSCUM CONTAGIOSUM VIRUS TYPES 1

TITLE OF INVENTION: AND 2

FILE REFERENCE: INDY:034

CURRENT APPLICATION NUMBER: US/09/133,521

CURRENT FILING DATE: 1998-08-18

EARLIER APPLICATION NUMBER: 60/055,532

EARLIER FILING DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 30

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 6

LENGTH: 92

TYPE: PRT

ORGANISM: Homo sapiens

3-09-133-521-6

Query Match

Best Local Similarity 100.0%; Score 486; DB 3; Length 92;

Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

/ 1 MKLCVTVLSLLMLVAAFCSPALSAPMGSDPPTACCFSTYARKLPRNFVVDYYETSSLCSQ 60

/ 1 MKLCVTVLSLLMLVAAFCSPALSAPMGSDPPTACCFSTYARKLPRNFVVDYYETSSLCSQ 60

/ 61 PAVVFQTKRSKQVCADPSESWSVQYVYDLELN 92

/ 61 PAVVFQTKRSKQVCADPSESWSVQYVYDLELN 92

## RESULT 8

3-08-679-493A-157

Sequence 157, Application US/08679493A

Patent No. 6303295

GENERAL INFORMATION:

APPLICANT: Taylor, Ethan W.

TITLE OF INVENTION: SELENOPROTEINS, CODING SEQUENCES AND METHODS

FILE REFERENCE: 55-95

CURRENT APPLICATION NUMBER: US/08/679,493A

CURRENT FILING DATE: 1996-07-12

PRIOR APPLICATION NUMBER: 60/001203

PRIOR FILING DATE: 1995-07-14

; PRIOR APPLICATION NUMBER: 60/003,112

; PRIOR FILING DATE: 1995-09-01

; NUMBER OF SEQ ID NOS: 216

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 157

; LENGTH: 92

; TYPE: PRT

; ORGANISM: Homo sapiens

US-08-679-493A-157

Query Match

Best Local Similarity 100.0%; Score 486; DB 4; Length 92;

Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLCVTVLSLLMLVAAFCSPALSAPMGSDPPTACCFSTYARKLPRNFVVDYYETSSLCSQ 60

Db 1 MKLCVTVLSLLMLVAAFCSPALSAPMGSDPPTACCFSTYARKLPRNFVVDYYETSSLCSQ 60

QY 61 PAVVFQTKRSKQVCADPSESWSVQYVYDLELN 92

Db 61 PAVVFQTKRSKQVCADPSESWSVQYVYDLELN 92

## RESULT 9

US-08-679-493A-158

; Sequence 158, Application US/08679493A

; Patent No. 6303295

; GENERAL INFORMATION:

; APPLICANT: Taylor, Ethan W.

; TITLE OF INVENTION: SELENOPROTEINS, CODING SEQUENCES AND METHODS

; FILE REFERENCE: 55-95

; CURRENT APPLICATION NUMBER: US/08/679,493A

; CURRENT FILING DATE: 1996-07-12

; PRIOR APPLICATION NUMBER: 60/001203

; PRIOR FILING DATE: 1995-07-14

; PRIOR APPLICATION NUMBER: 60/003,112

; PRIOR FILING DATE: 1995-09-01

; NUMBER OF SEQ ID NOS: 216

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 158

; LENGTH: 92

; TYPE: PRT

; ORGANISM: Homo sapiens

US-08-679-493A-158

Query Match

Best Local Similarity 100.0%; Score 486; DB 4; Length 92;

Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLCVTVLSLLMLVAAFCSPALSAPMGSDPPTACCFSTYARKLPRNFVVDYYETSSLCSQ 60

Db 1 MKLCVTVLSLLMLVAAFCSPALSAPMGSDPPTACCFSTYARKLPRNFVVDYYETSSLCSQ 60

QY 61 PAVVFQTKRSKQVCADPSESWSVQYVYDLELN 92

Db 61 PAVVFQTKRSKQVCADPSESWSVQYVYDLELN 92

## RESULT 10

US-09-230-371A-24

; Sequence 24, Application US/09230371A

; Patent No. 6348586

; GENERAL INFORMATION:

; APPLICANT: Chang, Yuan

; APPLICANT: Bohenzky, Roy A

; APPLICANT: Russo, James J

; APPLICANT: Edelman, Isidore S

; APPLICANT: Moore, Patrick S

; TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS SEQUENCES AND

; TITLE OF INVENTION: USES THEREOF

; FILE REFERENCE: 45185-G-PCT-US

; CURRENT APPLICATION NUMBER: US/09/230,371A

; CURRENT FILING DATE: 1999-11-17



PRIOR APPLICATION NUMBER: PCT/US97/13346  
PRIOR FILING DATE: 1997-07-22  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 24  
LENGTH: 92  
TYPE: PRT  
ORGANISM: Human  
S-09-230-371A-24

Query Match 100.0%; Score 486; DB 4; Length 92;  
Best Local Similarity 100.0%; Pred. No. 1.3e-50;  
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKLCVTVLSLLMLVAAFCSPPALSAPMGSDPPTACCFSTYARKLPNRFVVDYETSSLCSQ 60  
1 MKLCVTVLSLLMLVAAFCSPPALSAPMGSDPPTACCFSTYARKLPNRFVVDYETSSLCSQ 60

61 PAVVFQTKRSKQVCADPSESQVQYVVDLELN 92  
61 PAVVFQTKRSKQVCADPSESQVQYVVDLELN 92

## RESULT 11

S-08-808-720-7  
Sequence 7, Application US/08808720  
Patent No. 6100387

## GENERAL INFORMATION:

APPLICANT: Herrmann, Steve  
APPLICANT: Swanberg, Stephen  
TITLE OF INVENTION: CHIMERIC POLYPEPTIDES CONTAINING  
TITLE OF INVENTION: CHEMOKINE DOMAINS  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Genetics Institute, Inc.

STREET: 87 CambridgePark

CITY: Cambridge

STATE: MA

COUNTRY: USA

ZIP: 02140

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/808,720

FILING DATE:

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Sprunger, Suzanne

REGISTRATION NUMBER: P-41,323

REFERENCE/DOCKET NUMBER: GI5291

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 498-8284

TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 331 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

-08-808-720-7

Query Match 100.0%; Score 486; DB 3; Length 331;  
Best Local Similarity 100.0%; Pred. No. 6.4e-50;  
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKLCVTVLSLLMLVAAFCSPPALSAPMGSDPPTACCFSTYARKLPNRFVVDYETSSLCSQ 60  
1 MKLCVTVLSLLMLVAAFCSPPALSAPMGSDPPTACCFSTYARKLPNRFVVDYETSSLCSQ 60

QY 61 PAVVFQTKRSKQVCADPSESQVQYVVDLELN 92  
Db 61 PAVVFQTKRSKQVCADPSESQVQYVVDLELN 92

## RESULT 12

US-09-230-637-41

; Sequence 41, Application US/09230637

; Patent No. 6264958

; GENERAL INFORMATION:

; APPLICANT: Hayward, Gary

; APPLICANT: Nicholas, John

; APPLICANT: Hardwick, J. Marie

; APPLICANT: Reitz, Marvin

; TITLE OF INVENTION: No. 6264958el Genes of Kaposi's Sarcoma

; FILE REFERENCE: 1107.78372

; CURRENT APPLICATION NUMBER: US/09/230,637

; CURRENT FILING DATE: 1999-11-23

; PRIOR APPLICATION NUMBER: 60/022,591

; PRIOR FILING DATE: 1996-07-25

; PRIOR APPLICATION NUMBER: PCT US 97/12931

; PRIOR FILING DATE: 1997-07-24

; NUMBER OF SEQ ID NOS: 62

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 41

; LENGTH: 92

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-230-637-41

## Query Match

Best Local Similarity 99.2%; Score 482; DB 3; Length 92;

Matches 91; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKLCVTVLSLLMLVAAFCSPPALSAPMGSDPPTACCFSTYARKLPNRFVVDYETSSLCSQ 60  
Db 1 MKLCVTVLSLLMLVAAFCSPPALSAPMGSDPPTACCFSTYARKLPNRFVVDYETSSLCSQ 60

QY 61 PAVVFQTKRSKQVCADPSESQVQYVVDLELN 92

Db 61 PAVVFQTKRSKQVCADPSESQVQYVVDLELN 92

## RESULT 13

US-08-679-493A-159

; Sequence 159, Application US/08679493A

; Patent No. 6303295

; GENERAL INFORMATION:

; APPLICANT: Taylor, Ethan W.

; TITLE OF INVENTION: SELENOPROTEINS, CODING SEQUENCES AND METHODS

; FILE REFERENCE: 55-95

; CURRENT APPLICATION NUMBER: US/08/679,493A

; CURRENT FILING DATE: 1996-07-12

; PRIOR APPLICATION NUMBER: 60/001203

; PRIOR FILING DATE: 1995-07-14

; PRIOR APPLICATION NUMBER: 60/003,112

; PRIOR FILING DATE: 1995-09-01

; NUMBER OF SEQ ID NOS: 216

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 159

; LENGTH: 92

; TYPE: PRT

; ORGANISM: Homo sapiens

US-08-679-493A-159

Query Match 99.2%; Score 482; DB 4; Length 92;  
Best Local Similarity 98.9%; Pred. No. 3.9e-50;

Matches 91; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKLCVTVLSLLMLVAAFCSPPALSAPMGSDPPTACCFSTYARKLPNRFVVDYETSSLCSQ 60  
Db 1 MKLCVTVLSLLMLVAAFCSPPALSAPMGSDPPTACCFSTYARKLPNRFVVDYETSSLCSQ 60

/ 61 PAVVFQTKRSKQVCADPSESWSVQYVYVDLELN 92  
|||||  
5 61 PAVVFQTKRGKQVCADPSESWSVQYVYVDLELN 92

RESULT 14

3-07-792-988-2  
Sequence 2, Application US/07792988  
Patent No. 5306709

GENERAL INFORMATION:

APPLICANT: Gewirtz, Alan M.  
TITLE OF INVENTION: Suppression of megakaryo-  
TITLE OF INVENTION: cytopoiesis by macrophage inflammatory proteins  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: University of Pennsylvania

STREET: Suite 419  
STREET: 133 South 36th Street  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: U.S.A.  
ZIP: 19104-3246

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07792,988

FILING DATE: 19911115

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Monaco, Daniel A.

REGISTRATION NUMBER: 30,480

REFERENCE/DOCKET NUMBER: 6056-159

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-8383

TELEFAX: (215) 568-5549

TELEX: No. 5306709e

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 92 amino acids

TYPE: AMINO ACID

STRANDEDNESS: single stranded

TOPOLOGY: linear

3-07-792-988-2

Query Match 97.9%; Score 476; DB 1; Length 92;

Best Local Similarity 98.9%; Pred. No. 2e-49;

Matches 91; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

/ 1 MKLCVTVLSLLMLVAAFCSAPMSGSDPPTACCFSTARKLPNRFVVDYETSSLC SQ 60

|||||  
1 MKLCVTVLSLLMLVAAFCSLALSAPMSGSDPPTACCFSTARKLPNRFVVDYETSSLC SQ 60

/ 61 PAVVFQTKRSKQVCADPSESWSVQYVYVDLELN 92

|||||

/ 61 PAVVFQTKRSKQVCADPSESWSVQYVYVDLELN 92

RESULT 15

3-08-649-006A-9

Sequence 9, Application US/08649006A  
Patent No. 6548654

GENERAL INFORMATION:

APPLICANT: Hardiman, Gerard T.

APPLICANT: Rossi, Devora L.

APPLICANT: Bacon, Kevin B.

APPLICANT: Bazan, J. Fernando

/ APPLICANT: Schall, Thomas J.  
/ APPLICANT: Zlotnik, Albert  
/ TITLE OF INVENTION: Mammalian CX3C Chemokine Genes  
/ NUMBER OF SEQUENCES: 9  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: DNAX Research Institute  
/ STREET: 901 California Avenue  
/ CITY: Palo Alto  
/ STATE: California  
/ COUNTRY: USA  
/ ZIP: 94304-1104  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: PatentIn Release #1.0, Version #1.30  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/649,006A  
/ FILING DATE: 16-MAY-1996  
/ CLASSIFICATION: 536  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: US 08/590,828  
/ FILING DATE: 24-JAN-1996  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Ching, Edwin P.  
/ REGISTRATION NUMBER: 34,090  
/ REFERENCE/DOCKET NUMBER: DX0569K  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (650)852-9196  
/ TELEFAX: (650)496-1200  
/ INFORMATION FOR SEQ ID NO: 9:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 92 amino acids  
/ TYPE: amino acid  
/ STRANDEDNESS: not relevant  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: peptide  
/ US-08-649-006A-9

Query Match 94.9%; Score 461; DB 4; Length 92;  
Best Local Similarity 92.4%; Pred. No. 1.2e-47;  
Matches 85; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKLCVTVLSLLMLVAAFCSAPMSGSDPPTACCFSTARKLPNRFVVDYETSSLC SQ 60  
|||||  
Db 1 MKLCVSALSLLLVAAFCAPGFSAPMSGSDPPTSCCFSTARKLPNRFVVDYETSSLC SQ 60

QY 61 PAVVFQTKRSKQVCADPSESWSVQYVYVDLELN 92

|||||

Db 61 PAVVFQTKRSKQVCADPSESWSVQYVYVDLELN 92

Search completed: December 16, 2003, 15:40:17  
Job time : 14.5792 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

protein - protein search, using sw model

on: December 16, 2003, 15:36:20 ; Search time 13.4262 seconds  
(without alignments)  
651.810 Million cell updates/sec

le: US-09-920-137A-8

fect score: 478

quence: 1 MKVSAARLAVILIATLALCAP.....VCANPEKKWVREYINSLEMS 91

ring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

arched: 283308 seqs, 96168682 residues

al number of hits satisfying chosen parameters: 283308

imum DB seq length: 0  
imum DB seq length: 2000000000

it-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

abase : PIR 76:\*  
1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ult No.	Score	Query Match	Length	ID	Description
1	472	98.7	91	A28815	monocyte chemoattr
2	393	82.2	91	A46539	monocyte chemoattr
3	254.5	53.2	92	I46730	immune activation
4	252.5	52.8	93	B35673	LD78-beta protein
5	248	51.9	92	A30574	macrophage inflam
6	248	51.9	92	I52322	macrophage inflam
7	245.5	51.4	92	C30552	macrophage inflam
8	243	50.8	92	A32393	macrophage inflam
9	242.5	50.7	92	A31767	macrophage inflam
10	168	35.1	97	JC4912	eotaxin precursor
11	167	34.9	109	A54678	monocyte chemotact
12	162	33.9	120	I48147	monocyte chemoattr
13	156	32.6	148	S07723	immediate-early se
14	155	32.4	99	JC5295	monocyte chemotact
15	152	31.8	99	JC2136	monocyte chemoattr
16	148	31.0	50	C60407	monocyte adherence
17	147	30.8	97	A48093	monocytic cytokine
18	146.5	30.6	148	A30209	PDGF-inducible JE
19	144.5	30.2	120	JE0177	lymphocyte and mon
20	144	30.1	99	A39296	monocyte chemoattr
21	144	30.1	99	JC2336	monocyte chemoattr
22	143.5	30.0	99	JC2417	monocyte chemoattr
23	142	29.7	96	I48099	eotaxin precursor
24	141	29.5	96	JC2478	eotaxin precursor
25	140	29.3	99	A60299	monocyte chemoattr
26	140	29.3	125	I46857	monocyte chemoattr
27	125.5	26.3	116	I49555	gene C10 protein -
28	116	24.3	114	ETHUL	lymphotactin precu
29	107.5	22.5	92	S24236	TCA3 protein - mou

interleukin-8 prec  
cytokine SDF-1-bet  
interleukin-8 - do  
Neutrophil attract  
interleukin-8 prec  
interleukin-8 prec  
pre-B-cell growth-  
interleukin-8 homo  
cytokine - mouse  
I-309 protein precu  
lymphotactin precu  
interleukin-8 - ra  
monocyte chemotact  
transformation-ind  
RSV-induced protei  
hypothetical prote

ALIGNMENTS

RESULT 1

A28815

monocyte chemoattractant cytokine RANTES precursor - human

N;Alternate names: small inducible cytokine A5; T-cell specific cytokine RANTES  
C;Species: Homo sapiens (man)

C;Date: 30-Jun-1989 #sequence\_revision 16-Aug-1996 #text\_change 29-May-1998

C;Accession: A28815

R;Schall, T.J.; Jongstra, J.; Dyer, B.J.; Jorgensen, J.; Clayberger, C.; Davis, M.M.; K  
J. Immunol. 141, 1018-1025, 1988

A;Title: A human T cell-specific molecule is a member of a new gene family.

A;Reference number: A28815; MUID:88285659; PMID:2456327

A;Accession: A28815

A;Molecule type: mRNA

A;Residues: 1-91 <SCH>

A;Cross-references: GB:M21121

C;Comment: The acronym RANTES reflects the description "Regulated upon Activation, Norm  
C;Genetics:

A;Gene: GDB:SCYA5; D17S136E

A;Cross-references: GDB:120749; OMIM:187011

A;Map position: 17q11.2-17q12

C;Superfamily: macrophage inflammatory protein

C;Keywords: Chemotaxis; cytokine; immediate-early protein; inflammation; T-cell  
F;1-23/Domain: signal sequence #status predicted <SIG>

F;24-91/Product: T-cell protein RANTES #status predicted <MAT>

Query Match 98.7%; Score 472; DB 1; Length 91;  
Best Local Similarity 98.9%; Pred. No. 2.4e-44;  
Matches 90; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKVSAARLAVILIATLALCAPASAPSYSSDTPCCFAYIARPLPRAHIKEYFYTSKGKSNP 60

Db 1 MKVSAARLAVILIATLALCAPASAPSYSSDTPCCFAYIARPLPRAHIKEYFYTSKGKSNP 60

QY 61 AVFVTRKNRQVCANPEKKWVREYINSLEMS 91

Db 61 AVFVTRKNRQVCANPEKKWVREYINSLEMS 91

RESULT 2

A46539

monocyte chemoattractant cytokine RANTES precursor - mouse

N;Alternate names: Murantes

C;Species: Mus musculus (house mouse)

C;Date: 18-Jun-1993 #sequence\_revision 16-Aug-1996 #text\_change 22-Jun-1999

C;Accession: I48875; A46539; I48654; I56970

R;Danoff, T.M.; Lalley, P.A.; Chang, Y.S.; Heeger, P.S.; Neilson, E.G.

J. Immunol. 152, 1182-1189, 1994

A;Title: Cloning, genomic organization, and chromosomal localization of the Scya5 gene  
A;Reference number: I48875; MUID:94132613; PMID:7507961

A;Accession: I48875

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

[illegible]

RULT 3  
 1730  
 une activation gene 2 - rabbit  
 Species: Oryctolagus cuniculus (domestic rabbit)  
 Date: 14-Feb-1997 #sequence\_revision 14-Feb-1997 #text\_change 16-Jul-1999  
 Accession: I46730  
 Mori, S.; Goto, K.; Goto, F.; Mutakami, K.; Ohkawara, S.; Yoshinaga, M.  
 J. Immunol. 6, 149-156, 1994  
 Title: Dynamic changes in mRNA expression of neutrophils during the course of acute in  
 ference number: I46730; MUID:94198229; PMID:8148323  
 Accession: I46730  
 Status: preliminary; translated from GB/EMBL/DBJ  
 Molecule type: mRNA  
 Residues: 1-92 <MOR>  
 Cross-references: GB:D17402; NID:G599577; PIDN:BAA04226.1; PID:G599578  
 Superfamily: macrophage inflammatory protein

very Match 53.2%; Score 254.5; DB 2; Length 92;  
est Local Similarity 51.1%; Pred. No. 1.2e-20;  
atches 47; Conservative 16; Mismatches 28; Indels 1; Gaps 1;  
1 MKVSAARLAVILIATALCAPASAPYSSD-TTPCCFAYIARPLPRAHIKEYFYTSGKCSN 59

1 MKVSAARLAVILIATLAPASAPYSSD-TTPCCFAYIARPLPRAHIKEYFYTSGKCSN 59







crophage inflammatory protein-1-alpha precursor - mouse  
Alternate names: heparin-binding chemotaxis protein; L2G25B protein; SCI/MIP-1a; SIS a  
Species: Mus musculus (house mouse)  
Date: 17-Jul-1992 #sequence revision 17-Jul-1992 #text\_change 16-Jul-1999  
Accession: S11685; A32393; S04533; A53885; A30552; PS0303; A27596; I56104  
Grove, M.; Lowe, S.; Graham, G.; Pragnell, I.; Plumb, M.  
cleic Acids Res. 18, 5561, 1990  
Title: Sequence of the murine haemopoietic stem cell inhibitor/macrophage inflammatory  
Reference number: S11685; MUID:91016858; PMID:2216738  
Accession: S11685  
Molecule type: DNA  
Residues: 1-92 <GRO>  
Cross-references: EMBL:X53372; NID:G54062; PIDN:CAA37452.1; PID:G297531  
Note: the authors' translation of the nucleotide sequence differs at several positions  
Kwon, B.S.; Weissman, S.M.  
oc. Natl. Acad. Sci. U.S.A. 86, 1963-1967, 1989  
Title: cDNA sequence of two inducible T-cell genes.  
Reference number: A32393; MUID:89184547; PMID:2784565  
Accession: A32393  
Molecule type: mRNA  
Residues: 1-92 <KWO>  
Cross-references: GB:J04491; NID:G201524; PIDN:AAA40304.1; PID:G201525  
Davatelis, G.; Tekamp-Olson, P.; Wolpe, S.D.; Hermesen, K.; Luedke, C.; Gallegos, C.;  
Exp. Med. 167, 1939-1944, 1988  
Title: Cloning and characterization of a cDNA for murine macrophage inflammatory protei  
Reference number: S04533; MUID:88258380; PMID:3290382  
Accession: S04533  
Molecule type: mRNA  
Residues: 1-48, 'E', 50-90, 'I', 92 <DA2>  
Cross-references: EMBL:X12531  
Note: the authors translated the codon GAG for residue 49 as Asp and ATT for residue 9  
Note: the sequence has been corrected in reference A53885  
Davatelis, G.; Tekamp-Olson, P.; Wolpe, S.D.; Hermesen, K.; Luedke, C.; Gallegos, C.;  
Exp. Med. 170, 2189, 1989  
Reference number: A53885  
Contents: erratum  
Accession: A53885  
Molecule type: mRNA  
Residues: 1-92 <DAV>  
Cross-references: EMBL:X12531; NID:G53122; PIDN:CAA31047.1; PID:G53123  
Brown, K.D.; Zurawski, S.M.; Mosmann, T.R.; Zurawski, G.  
Immunol. 142, 679-687, 1989  
Title: A family of small inducible proteins secreted by leukocytes are members of a ne  
of various activation processes.  
Reference number: A30552; MUID:89093958; PMID:2521353  
Accession: A30552  
Molecule type: mRNA  
Residues: 1-21, 'L', 23-61, 'A', 63-92 <BRO>  
Cross-references: GB:M23447; NID:G533240; PIDN:AAA40146.1; PID:G533241  
Sherry, B.; Tekamp-Olson, P.; Gallegos, C.; Bauer, D.; Davatelis, G.; Wolpe, S.D.; Mas  
Exp. Med. 168, 2251-2259, 1988  
Title: Resolution of the two components of macrophage inflammatory protein 1, and clon  
Reference number: J10088; MUID:89067830; PMID:3058856  
Accession: PS0303  
Molecule type: mRNA  
Residues: 24-33, 'XX', 36-54 <SHE>  
Wolpe, S.D.; Davatelis, G.; Sherry, B.; Beutler, B.; Hesse, D.G.; Nguyen, H.T.; Moldaw  
Exp. Med. 167, 570-581, 1988  
Title: Macrophages secrete a novel heparin-binding protein with inflammatory and neutr  
Reference number: A27596; MUID:88154745; PMID:3279154  
Accession: A27596  
Molecule type: protein  
Residues: 24-33, 'XX', 36-42 <WOL>  
Note: 26-Met, 30-Pro, and 39-Thr were also found  
Widmer, U.; Yang, Z.; van Deventer, S.; Manogue, K.R.; Sherry, B.; Cerami, A.  
Immunol. 146, 4031-4040, 1991  
Title: Genomic structure of murine macrophage inflammatory protein-1-alpha and conserv  
Reference number: I56104; MUID:91237116; PMID:2033269  
Accession: I56104  
Status: preliminary; translated from GB/EMBL/DBJ  
Molecule type: DNA  
Residues: 1-92 <RES>  
Cross-references: GB:M73061; NID:G199694; PIDN:AAA39707.1; PID:G199695

C:Comment: This protein is a monokine.

C:Genetics:

A:Introns: 23/3; 26/1; 63/2

C:Superfamily: macrophage inflammatory protein

C:Keywords: heparin binding

F:1-23/Domain: signal sequence #status predicted <SIG>

F:24-92/Product: macrophage inflammatory protein #status experimental <MAT>

Query Match 50.8%; Score 243; DB 2; Length 92;

Best Local Similarity 48.9%; Pred. No. 2.le-19;

Matches 45; Conservative 19; Mismatches 26; Indels 2; Gaps 2;

QY 1 MKVSAARLAVILIATALCAPASAPYSSDT-TPCCFAYIARPLPRAHIKEYFYTSKCSN 59

Db 1 MKVSTTALAVLLCTMTLCNQVFSAPYGADTPTACCFSY-SRKIPQFIVDYFETSSLSQ 59

QY 60 PAVVFTRKNRQVCANPEKKWVREYINSLEMS 91

Db 60 PGVIFLTRNRQICADSKETWQVEYITDLELN 91

#### RESULT 9

A31767

macrophage inflammatory protein 1-beta precursor [validated] - human

N;Alternate names: cytokine HC21; G-26 protein; H400 homolog; lymphocyte activation ge  
protein 2 (Act-2); T-cell activation protein gamma

C:Species: Homo sapiens (man)

C>Date: 07-Jun-1990 #sequence revision 29-May-1998 #text change 15-Sep-2000

C;Accession: JH0319; A40978; A31767; A37411; B30574; B45817; D30552

R;Baixeras, E.; Roman-Roman, S.; Jitsukawa, S.; Genevee, C.; Mechiche, S.; Viegas-Pegu

Mol. Immunol. 27, 1091-1102, 1990

A;Title: Cloning and expression of a lymphocyte activation gene (LAG-1).

A;Reference number: JH0319; MUID:91061800; PMID:2247088

A;Accession: JH0319

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-92 <BAI>

A;Cross-references: GB:X53682; NID:G34217; PIDN:CAA37723.1; PID:G34218

A;Experimental source: natural killer cell, strain CD3-CD2+, F5, SIIIE5

R;Napolitano, M.; Modi, W.S.; Cevario, S.J.; Gnarr, J.R.; Seuanez, H.N.; Leonard, W.J

J. Biol. Chem. 266, 17531-17536, 1991

A;Title: The gene encoding the Act-2 cytokine. Genomic structure, HTLV-I/tax responsiv

A;Reference number: A40978; MUID:91373378; PMID:1894635

A;Accession: A40978

A;Molecule type: DNA

A;Residues: 1-14, 'S', 16-69, 'G', 71-92 <NAP>

A;Cross-references: GB:M69201; NID:G178021

A;Note: 15-Ala was also found

R;Lipes, M.A.; Napolitano, M.; Jeang, K.T.; Chang, N.T.; Leonard, W.J.

Proc. Natl. Acad. Sci. U.S.A. 85, 9704-9708, 1988

A;Title: Identification, cloning, and characterization of an immune activation gene.

A;Reference number: A31767; MUID:89071764; PMID:2462251

A;Accession: A31767

A;Molecule type: mRNA

A;Residues: 1-92 <LIP>

A;Cross-references: GB:J04130; NID:G178017; PIDN:AAA51576.1; PID:G178018

R;Chang, H.C.; Reinherz, E.L.

Eur. J. Immunol. 19, 1045-1051, 1989

A;Title: Isolation and characterization of a cDNA encoding a putative cytokine which i

A;Reference number: A37411; MUID:89325421; PMID:2568930

A;Accession: A37411

A;Molecule type: mRNA

A;Residues: 1-92 <CHA>

A;Cross-references: GB:X16166; NID:G32035; PIDN:CAA34291.1; PID:G32036

R;Zipfel, P.F.; Balke, J.; Irving, S.G.; Kelly, K.; Siebenlist, U.

J. Immunol. 142, 1582-1590, 1989

A;Title: Mitogenic activation of human T cells induces two closely related genes which

A;Reference number: A30574; MUID:89140347; PMID:2521882

A;Accession: B30574

A;Molecule type: mRNA

A;Residues: 1-19, 'L', 21-92 <ZIP>

A;Cross-references: GB:M25316; NID:G602454; PIDN:AAA57256.1; PID:G602455

R;Miller, M.D.; Hata, S.; Malefyt, R.D.W.; Krangel, M.S.

Immunol. 143, 2907-2916, 1989

Title: A novel polypeptide secreted by activated human T lymphocytes.

Reference number: A45817; MUID:90038522; PMID:2809212

Accession: B45817

Molecule type: mRNA

Residues: 7-55, 'I', 57-79, 'T', 81-92 <MIL>

Cross-references: GB:M57503; NID:g339726; PIDN:AAA36752.1; PID:g339727

Brown, K.D.; Zurawski, S.M.; Mosmann, T.R.; Zurawski, G.

Immunol. 142, 679-687, 1989

Title: A family of small inducible proteins secreted by leukocytes are members of a new family of various activation processes.

Reference number: A30552; MUID:89093958; PMID:2521353

Accession: D30552

Molecule type: mRNA

Residues: 1-39, 'REASS', 46-92 <BRO>

Cross-references: GB:M23502; NID:g533212; PIDN:AAA36656.1; PID:g533213

Clore, G.M.; Lodi, P.J.; Garrett, D.S.; Groenenborn, A.M.

Submitted to the Brookhaven Protein Data Bank, January 1994

Reference number: A52206; PDB:1HUM

Contents: annotation; conformation and disulfide bond assignments by (1)H-NMR, residue

Comment: This protein is secreted by activated lymphocytes and monocytes. It is bound

Genetics:

Gene: GDB:LAG1

Cross-references: GDB:127451; OMIM:153335

Map position: 17q21-17q21

Introns: 26/1; 64/2

Superfamily: macrophage inflammatory protein

Keywords: Chemotaxis; cytokine; inflammation

1-23/Domain: signal sequence #status predicted <SIG>

24-92/Product: macrophage inflammatory protein 1-beta #status experimental <MAT>

34-58,35-74/Disulfide bonds: #status experimental

Query Match 50.7%; Score 242.5; DB 1; Length 92;

Best Local Similarity 45.7%; Pred. No. 2.3e-19;

Matches 42; Conservative 23; Mismatches 26; Indels 1; Gaps 1;

1 MKVSAARLAVILLIATLALCAPASAPYSSD-TTPCCFAYIARPLPRAHIKEYFTSGKCSN 59

||||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||

1 MKLCVTLSLLMLVAECPALSPMGSDPPTACCFSTARKLPNFFVVDYETSSLSQ 60

60 PAWVFTRKRNQVCANPEKKWVREYINSLEMS 91

||||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||

61 PAWVFQTKRSKQVCADPSWSVQYVYDLELN 92

RESULT 10

J4912

taxin precursor - human

Species: Homo sapiens (man)

Date: 01-Nov-1996 #sequence\_revision 01-Nov-1996 #text\_change 20-Jun-2000

Accession: JC4912

Bartels, J.; Schlueter, C.; Richter, E.; Noso, N.; Kulke, R.; Christophers, E.; Schroeder, C.

ochem. Biophys. Res. Commun. 225, 1045-1051, 1996

Title: Human dermal fibroblasts express eotaxin: Molecular cloning, mRNA expression, a

Reference number: JC4912; MUID:96374440; PMID:8780731

Accession: JC4912

Status: preliminary

Molecule type: mRNA

Residues: 1-97 <BAR>

Cross-references: EMBL:Z75669; NID:g1531982; PIDN:CAA99997.1; PID:g1531983

Experimental source: dermal fibroblast

Comment: This protein has eosinophil specific chemotactic activity.

Superfamily: macrophage inflammatory protein

Keywords: fibroblast

1-18/Domain: signal sequence #status predicted <SIG>

19-97/Product: eotaxin #status predicted <MAT>

Query Match 35.1%; Score 168; DB 2; Length 97;

Best Local Similarity 41.1%; Pred. No. 3.2e-11;

Matches 37; Conservative 16; Mismatches 35; Indels 2; Gaps 2;

1 MKVSAARLAVILLIATLALCAPASAPYSSD-TTPCCFAYIARPLPRAHIKEY-FYTSKCSN 59

||||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||

```

Db      1 MKVSAALLWLLIAAASPQGLTGPASVPTT-CCFNLANRKIPLQRLSEYRRITSGKCPQ 59

QY      60 PAVVVFVTRKNRQVCANPEKKWVREYINSLE 89
      ||:| | : : ||:| | : : ||:| | : :
Db      60 XAVIEFTKLAKDICADPKKRWVQDSMKYLD 89

RESULT 11
A54678
monocyte chemotactic protein 3 precursor - human
N;Alternate names: monocyte chemoattractant protein MCP-3
C;Species: Homo sapiens (man)
C;Date: 28-Oct-1994 #sequence revision 28-Oct-1994 #text_change 16-Jul-1999
C;Accession: A54678; JCI1478; S32222
R;Opdenakker, G.; Fiten, P.; Nys, G.; Froyen, G.; Van Roy, N.; Speleman, F.; Laureys,
Genomics 21, 403-408, 1994
A;Title: The human MCP-3 gene (SCYA7): cloning, sequence analysis, and assignment to
A;Reference number: A54678; MUID:94375065; PMID:7916328
A;Accession: A54678
A;Molecule type: DNA
A;Residues: 1-109 <OPD>
A;Cross-references: GB:X72309
R;Opdenakker, G.; Froyen, G.; Fiten, P.; Proost, P.; Van Damme, J.
Biochem. Biophys. Res. Commun. 191, 535-542, 1993
A;Title: Human monocyte chemotactic protein-3 (MCP-3): Molecular cloning of the cDNA
A;Reference number: JCI1478; MUID:93213290; PMID:8461011
A;Accession: JCI1478
A;Molecule type: mRNA
A;Residues: 1-109 <OP2>
A;Cross-references: GB:X72308; GB:S57464; NID:g3928270; PIDN:CAA51055.1; PID:g313708
R;Minty, A.; Chalon, P.; Guillemot, J.C.; Kaghad, M.; Liauzun, P.; Magazin, M.; Milou
submitted to the EMBL Data Library, March 1993
A;Description: Molecular cloning of MCP-3: a human monocyte-derived monocyte chemoat
A;Reference number: S32222
A;Accession: S32222
A;Molecule type: mRNA
A;Residues: 1-109 <MIN>
A;Cross-references: EMBL:X71087; NID:g288396; PIDN:CAA50405.1; PID:g288397
C;Comment: This protein induces proteinase secretion and chemotaxis by macrophages an
C;Genetics:
A;Gene: GDB:SCYA7; SCYA6; MCP-3
A;Cross-references: GDB:138473; OMIM:158106
A;Map position: 17q11-17q12
A;Introns: 36/1; 75/2
C;Superfamily: macrophage inflammatory protein
C;Keywords: cytokine; glycoprotein; inflammation
F;1-33/Domain: signal sequence #status predicted <SIG>
F;34-109/Product: monocyte chemotactic protein 3 #status predicted <MAT>
F;39/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match      34.9%; Score 167; DB 2; Length 109;
Best Local Similarity 35.2%; Pred. No. 4.5e-11;
Matches 32; Conservative 23; Mismatches 34; Indels 2; Gaps 2;

QY      1 MKVSAARLAVILIATLALCAPASAPSYSSDT-TPCCFAYIARPLPRAHIKEY-FYTSKCS 58
      ||| ||| | : : | | | | | : | | | | : | | | | : | | | | : | | | | : | | | |
Db      11 MKASAALLCLLLTAAPSPQGLAQPVGINTSTTCYRFINKKIPKQRLSEYRRITSSHCP 70

QY      59 NPVVVFVTRKNRQVCANPEKKWVREYINSLE 89
      ||:| | : : ||:| | : : ||:| | : : ||:| | : :
Db      71 REAVIEFTKLDKEICADPTQKWVQDFMKHLD 101

RESULT 12
I48147
monocyte chemoattractant protein-1 - guinea pig
C;Species: Cavia porcellus (guinea pig)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
C;Accession: I48147
R;Yoshimura, T.
J. Immunol. 150, 5025-5032, 1993
A;Title: cDNA cloning of guinea pig monocyte chemoattractant protein-1 and expression
A;Reference number: I48147; MUID:93267104; PMID:8496603

```

[illegible]



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

protein - protein search, using sw model

1 on: December 16, 2003, 15:36:20 ; Search time 10.4426 Seconds  
(without alignments)  
409.804 Million cell updates/sec

le: US-09-920-137A-8

fect score: 478

quence: 1 MKVSAARLAVILIATCAP.....VCANPEKKWREYINSLEMS 91

oring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

arched: 127863 segs, 47026705 residues

al number of hits satisfying chosen parameters: 127863

imum DB seq length: 0

imum DB seq length: 2000000000

it-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

abase : SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

ult No.	Score	Query Match	Length	DB	ID	Description
1	472	98.7	91	1	SY05_HUMAN	P13501 homo sapien
2	416	87.0	91	1	SY05_CAVPO	P97272 cavia porce
3	404	84.5	91	1	SY05_BOVIN	O97919 bos taurus
4	393	82.2	91	1	SY05_MOUSE	P30882 mus musculu
5	383.5	80.2	92	1	SY05_RAT	P50231 rattus norv
6	372	77.8	91	1	SY05_SIGHI	Q91211 sigmodon hi
7	254.5	53.2	92	1	SY04_RABIT	P46632 oryctolagus
8	252.5	52.8	93	1	SY3L_HUMAN	P16619 homo sapien
9	251.5	52.6	90	1	SY04_CHICK	Q90826 gallus gall
10	248	51.9	92	1	SY03_HUMAN	P10147 homo sapien
11	248	51.9	92	1	SY03_RAT	P50229 rattus norv
12	245.5	51.4	92	1	SY04_MOUSE	P14097 mus musculu
13	243	50.8	92	1	SY03_MOUSE	P10855 mus musculu
14	242.5	50.7	92	1	SY04_HUMAN	P13236 h small ind
15	228.5	47.8	92	1	SY04_RAT	P50230 rattus norv
16	218	45.6	50	1	SY05_PIG	Q29288 sus scrofa
17	186	38.9	93	1	SY14_HUMAN	Q16627 homo sapien
18	182.5	38.2	89	1	SY18_HUMAN	P55774 h small ind
19	178.5	37.3	92	1	SY22_MOUSE	O88430 mus musculu
20	175	36.6	97	1	EOTA_HUMAN	P51671 homo sapien
21	174.5	36.5	94	1	SY26_HUMAN	Q9Y258 homo sapien
22	167	34.9	99	1	SY07_HUMAN	P80098 homo sapien
23	165.5	34.6	120	1	SY23_HUMAN	P55773 homo sapien
24	162	33.9	120	1	SY02_CAVPO	Q08782 cavia porce
25	159.5	33.4	98	1	SY13_HUMAN	Q99616 homo sapien
26	158	33.1	113	1	SY15_HUMAN	Q16663 homo sapien
27	157.5	32.9	120	1	SY16_HUMAN	O15467 h small ind
28	156	32.6	97	1	SY07_RAT	Q9QXY8 rattus norv
29	156	32.6	99	1	SY08_HUMAN	P80075 homo sapien
30	156	32.6	148	1	SY02_RAT	P14844 rattus norv
31	155	32.4	94	1	VM12_KSHV	Q98157 kaposi's sa
32	154	32.2	97	1	EOTA_RAT	P97545 rattus norv
33	152	31.8	97	1	SY07_MOUSE	Q03366 mus musculu

RESULT 1

SY05\_HUMAN STANDARD; PRT; 91 AA.

AC P13501; O43646; Q9NYA2;

DT 01-JAN-1990 (Rel. 13, Created)

DT 15-JUL-1999 (Rel. 38, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Small inducible cytokine A5 precursor (CCL5) (T-cell specific RANTES

protein) (SIS-delta) (T cell-specific protein P228) (TCP228).

DE CCL5 OR SCYA5.

GN Homo sapiens (Human).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=88285659; PubMed=2456327;

RA Schall T.J., Jongstra J., Dyer B.J., Jorgensen J., Clayberger C.,

RA Davis M.M., Krensky A.M.;

RT "A human T cell-specific molecule is a member of a new gene family.";

RL J. Immunol. 141:1018-1025(1988).

RN [2]

RP SEQUENCE FROM N.A.

RA Jang J.S., Kim B.E.;

RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=92228475; PubMed=10213461;

RA Nomiyama H., Fukuda S., Iio M., Tanase S., Miura R., Yoshie O.;

RT "Organization of the chemokine gene cluster on human chromosome

17q11.2 containing the genes for CC chemokine MPIF-1, HCC-2, LEC, and

RT RANTES.";

RL J. Interferon Cytokine Res. 19:227-234(1999).

RN [4]

RP SEQUENCE FROM N.A.

RA Zeng Q.P., Yang R.Y., Fu L.C.;

RL "The complete sequence of human beta-chemokine RANTES mRNA.";

Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.

RN [5]

RP SEQUENCE FROM N.A.

TISSUE=Brain;

RA MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

ALIGNMENTS

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002). [6]

SEQUENCE OF 49-56; 71-79 AND 83-91, AND FUNCTION. MEDLINE=96106406; PubMed=8525373; Cocchi F., DeVico A.L., Garzino-Demo A., Arya S.K., Gallo R.C., Lusso P.; "Identification of RANTES, MIP-1 alpha, and MIP-1 beta as the major HIV-suppressive factors produced by CD8+ T cells."; Science 270:1811-1815(1995). [7]

STRUCTURE BY NMR. MEDLINE=95352612; PubMed=7542919; Chung C.-W., Cooke R.M., Proudfoot A.E.I., Wells T.N.C.; "The three-dimensional solution structure of RANTES."; Biochemistry 34:9307-9314(1995). [8]

STRUCTURE BY NMR. MEDLINE=95244456; PubMed=7537088; Skelton N.J., Aspiras F., Ogez J., Schall T.J.; "Proton NMR assignments and solution conformation of RANTES, a chemokine of the C-C type."; Biochemistry 34:5329-5342(1995). [9]

SYNTHESIS, AND X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS). MEDLINE=99111238; PubMed=989151; Wilken J., Hoover D., Thompson D.A., Barlow P.N., McSparron H., Picard L., Wlodawer A., Lubkowski J., Kent S.B.; "Total chemical synthesis and high-resolution crystal structure of the potent anti-HIV protein AOP-RANTES."; Chem. Biol. 6:43-51(1999). [10]

X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS). Hoover D.M., Shaw J., Gryczynski Z., Proudfoot A.E.I., Wells T.N.C., Lubkowski J.; "The crystal structure of Met-RANTES: comparison with native RANTES and AOP-RANTES."; Protein Pept. Lett. 7:73-82(2000).

-!- FUNCTION: CHEMOATTRACTANT FOR BLOOD MONOCYTES, MEMORY T HELPER CELLS AND EOSINOPHILS. CAUSES THE RELEASE OF HISTAMINE FROM BASOPHILS AND ACTIVATES EOSINOPHILS. BINDS TO CCR1, CCR3, CCR4 AND CCR5. ONE OF THE MAJOR HIV-SUPPRESSIVE FACTORS PRODUCED BY CD8+ T CELLS. RECOMBINANT RANTES PROTEIN INDUCES A DOSE-DEPENDENT INHIBITION OF DIFFERENT STRAINS OF HIV-1, HIV-2, AND SIMIAN IMMUNODEFICIENCY VIRUS (SIV).

-!- SUBCELLULAR LOCATION: Secreted.

-!- TISSUE SPECIFICITY: T-CELL AND MACROPHAGE SPECIFIC.

-!- INDUCTION: By mitogens.

-!- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE C-C) (CHEMOKINE CC).

-----

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

-----

EMBL; M21121; AAA36725.1; -.

EMBL; AF043341; AAC03541.1; -.

EMBL; AF088219; AAC63331.1; -.

EMBL; AF266753; AAF73070.1; -.

EMBL; BC008600; AAH08600.1; -.

PIR; A28815; A28815.

PDB; 1HRJ; 14-OCT-96.

PDB; 1RTN; 03-JUN-95.

PDB; 1RTO; 03-JUN-95.

PDB; 1B3A; 23-APR-99.

PDB; 1EQT; 19-APR-00.

Genew; HGNC:10632; CCL5.

MIM; 187011; -.

GO; GO:0003800; F:antiviral response protein activity; TAS.

GO; GO:0008009; F:chemokine activity; TAS.

GO; GO:0006874; P:calcium ion homeostasis; TAS.

GO; GO:0007155; P:cell adhesion; TAS.

GO; GO:0006928; P:cell motility; TAS.

GO; GO:0007267; P:cell-cell signaling; TAS.

GO; GO:0006968; P:cellular defense response; TAS.

GO; GO:0006935; P:chemotaxis; TAS.

GO; GO:0006887; P:exocytosis; TAS.

GO; GO:0006954; P:inflammatory response; TAS.

GO; GO:0006979; P:response to oxidative stress; TAS.

GO; GO:0009615; P:response to viruses; TAS.

GO; GO:0007165; P:signal transduction; TAS.

InterPro; IPR000827; CC Chemokine sml.

InterPro; IPR001811; Chemokine\_IL8.

Pfam; PF00048; IL8; 1.

SMART; SM00199; SCY; 1.

PROSITE; PS00472; SMALL CYTOKINES\_CC; 1.

Cytokine; Chemotaxis; T-cell; Signal; Inflammatory response; 3D-structure.

KW SIGNAL 1 23

FT CHAIN 24 91 SMALL INDUCIBLE CYTOKINE A5.

FT DISULFID 33 57

FT DISULFID 34 73

FT CONFLICT 7 7

FT CONFLICT 14 14

FT STRAND 30 33

FT HELIX 44 46

FT STRAND 47 52

FT TURN 55 56

FT STRAND 62 66

FT TURN 67 68

FT STRAND 71 74

FT TURN 76 77

FT HELIX 79 91

SQ SEQUENCE 91 AA; 9990 MW; FB0BFAF9A87C620F CRC64;

Query Match 98.7%; Score 472; DB 1; Length 91;

Best Local Similarity 98.9%; Pred. No. 7.3e-46;

Matches 90; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

A -> R (IN REF. 1 AND 4).

A -> V (IN REF. 4).

QY 1 MKVSAARLAVILIATALCAPASASPYSSDTPCCFAYIARPLPRAHIKEYFTSGKSNP 60

Db 1 MKVSAARLAVILIATALCAPASASPYSSDTPCCFAYIARPLPRAHIKEYFTSGKSNP 60

QY 61 AVVFVTRKNQVCANPEKKWVREYINSLEMS 91

Db 61 AVVFVTRKNQVCANPEKKWVREYINSLEMS 91

RESULT 2

SY05\_CAVPO STANDARD; PRT; 91 AA.

ID SY05\_CAVPO

AC P97272; O09076;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Small inducible cytokine A5 precursor (CCL5) (T-cell specific RANTES protein) (SIS-delta).

DE CCL5 OR SCYAS.

OS Cavia porcellus (Guinea pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Euthera; Rodentia; Hystricognathi; Caviidae; Cavia.

OX NCBI\_TaxID=10141;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Dunkin-Hartley;

RA Campbell E.M., Proudfoot A.E.I., Yoshimura T., Allet B., Wells T.N.C., White A.M., Westwick J., Watson M.L.;

RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.



```
[2]
SEQUENCE FROM N.A.
TISSUE=Lung;
Asano K., Nakamura M., Oguma T., Fukunaga K., Ishizaka A.,
Yamaguchi K., Kanazawa M.;
Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
-!- FUNCTION: CHEMOATTRACTANT FOR BLOOD MONOCYTES, MEMORY T HELPER
CELLS AND EOSINOPHILS. CAUSES THE RELEASE OF HISTAMINE FROM
BASOPHILS AND ACTIVATES EOSINOPHILS (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
C-C) (CHEMOKINE CC).
-----
This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
-----
EMBL; U77037; AAC53293.1; -.
EMBL; AB002662; BAA19604.1; -.
HSSP; P13501; 1RTN.
InterPro; IPR000827; CC_chemkine_sml.
InterPro; IPR001811; Chemokine_IL8.
Pfam; PF00048; IL8; 1.
SMART; SM00199; SCY; 1.
PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
Cytokine; Chemotaxis; T-cell; Signal; Inflammatory response.
SIGNAL 1 23 POTENTIAL.
CHAIN 24 91 SMALL INDUCIBLE CYTOKINE A5.
DISULFID 33 57 BY SIMILARITY.
DISULFID 34 73 BY SIMILARITY.
SEQUENCE 91 AA; 10088 MW; 7F6A31B751237DB9 CRC64;

Query Match 87.0%; Score 416; DB 1; Length 91;
Best Local Similarity 86.8%; Pred. No. 1.3e-39;
Matches 79; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

1 MKVSAARLAVILIATLALCAPASASPYSDTTPCCFAYIARPLPRAHIKEYFYTSKCSNP 60
1 MKVSAALCVILTTAALCVPASASPYASDTTPCCFAYISRALPRTHIKEYFYTSKCSNL 60

61 AVFVTRKNRQVCANPEKKWVREYINSLEMS 91
61 AVFVTRKNRQVCANPEKKWVREYINSLEMS 91

ULT 3
5 BOVIN
-SY05_BOVIN STANDARD; PRT; 91 AA.
O97919;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Small inducible cytokine A5 precursor (CCL5) (T-cell specific RANTES
protein) (SIS-delta).
CCL5 OR SCYA5.
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
[1]
SEQUENCE FROM N.A.
TISSUE=Intestine;
Aust G., Thamm B., Rost A.K.;
"Cloning of Bos taurus RANTES mRNA.";
Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
-!- FUNCTION: CHEMOATTRACTANT FOR BLOOD MONOCYTES, MEMORY T HELPER
CELLS AND EOSINOPHILS. CAUSES THE RELEASE OF HISTAMINE FROM
BASOPHILS AND ACTIVATES EOSINOPHILS (BY SIMILARITY).
```

```
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
CC C-C) (CHEMOKINE CC).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AJ007043; CAA07430.1; -.
CC HSSP; P13501; 1RTN.
CC InterPro; IPR000827; CC_chemkine_sml.
CC InterPro; IPR001811; Chemokine_IL8.
CC Pfam; PF00048; IL8; 1.
CC SMART; SM00199; SCY; 1.
CC PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
CC Cytokine; Chemotaxis; T-cell; Signal; Inflammatory response.
KW SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 91 SMALL INDUCIBLE CYTOKINE A5.
FT DISULFID 33 57 BY SIMILARITY.
FT DISULFID 34 73 BY SIMILARITY.
SQ SEQUENCE 91 AA; 10073 MW; 660DD38E015B0735 CRC64;

Query Match 84.5%; Score 404; DB 1; Length 91;
Best Local Similarity 80.2%; Pred. No. 2.7e-38;
Matches 73; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

1 MKVSAARLAVILIATLALCAPASASPYSDTTPCCFAYIARPLPRAHIKEYFYTSKCSNP 60
1 MKVSATAFAVLLMAAALCAPASASPYASDTTPCCFAYISRPLPRTHVQYFYTSKCSMA 60

61 AVFVTRKNRQVCANPEKKWVREYINSLEMS 91
61 AVFVTRKNRQVCANPEKKWVREYINSLEMS 91

RESULT 4
SY05_MOUSE
ID -SY05_MOUSE STANDARD; PRT; 91 AA.
AC P30882;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Small inducible cytokine A5 precursor (CCL5) (T-cell specific RANTES
DE protein) (SIS-delta) (MuRantes).
GN CCL5 OR SCYA5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92277990; PubMed=1375672;
RA Heeger P., Wolf G., Meyers C., Sun M.J., O'Farrell S.C.,
RA Krensky A.M., Neilson E.G.;
RT "Isolation and characterization of cDNA from renal tubular epithelium
RT encoding murine Rantes.";
RL Kidney Int. 41:220-225(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92289805; PubMed=1376260;
RA Schall T.J., Simpson N.J., Mak J.Y.;
RT "Molecular cloning and expression of the murine RANTES cytokine:
RT structural and functional conservation between mouse and man.";
RL Eur. J. Immunol. 22:1477-1481(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=NIH Swiss;
RX MEDLINE=94132613; PubMed=7507961;
RA Danoff T.M., Lailey P.A., Chang Y.S., Heeger P.S., Neilson E.G.;
```







Query Match 52.8%; Score 252.5; DB 1; Length 93;  
Best Local Similarity 47.8%; Pred. No. 2.1e-21;  
Matches 44; Conservative 25; Mismatches 22; Indels

Best Local Similarity 51.1%; Pred. No. 2.6e-21;  
Matches 47; Conservative 19; Mismatches 23; Indels 3; Gaps 2;  
QY 1 MKVSAARLAVILLIATALCAPASASPYSSD-TTPCCFAYIARPLPRAHIKEYFYTSKCSN 59  
Db 1 MKVSVAAALAVLLI--AICYQTSAAAPVGSDDPTSCCTYISRLPFFSVADYYETNSQCPH 58  
QY 60 PAVVFTVRKNRQVCANPEKKWVREYINSLEMS 91  
Db 59 AGVVFITRKGREVCANPNDWVDYMKMELN 90

RESULT 10  
SY03\_HUMAN STANDARD; PRT; 92 AA.  
AC P10147;  
DT 01-MAR-1989 (Rel. 10, Created)  
DT 01-MAR-1989 (Rel. 10, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Small inducible cytokine A3 precursor (CCL3) (Macrophage inflammatory  
protein 1-alpha) (MIP-1-alpha) (Tonsillar lymphocyte LD78 alpha  
protein) (GO/GI switch regulatory protein 19-1) (GOS19-1 protein)  
DE (SIS-beta) (PAT 464.1).  
GN CCL3 OR SCYA3 OR GOS19-1 OR MIP1A.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=86223879; PubMed=3086300;  
RA Obaru K., Fukuda M., Maeda S., Shimada K.;  
RT "A cDNA clone used to study mRNA inducible in human tonsillar  
lymphocytes by a tumor promoter."  
RL J. Biochem. 99:885-894(1986).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89140347; PubMed=2521882;  
RA Zipfel P.F., Balke J., Irving S.G., Kelly K., Siebenlist U.;  
RT "Mitogenic activation of human T cells induces two closely related  
genes which share structural similarities with a new family of  
secreted factors."  
RL J. Immunol. 142:1582-1590(1989).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91103879; PubMed=2271120;  
RA Blum S., Forsdyke R.E., Forsdyke D.R.;  
RT "Three human homologs of a murine gene encoding an inhibitor of stem  
cell proliferation."  
RL DNA Cell Biol. 9:589-602(1990).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90287155; PubMed=1694014;  
RA Nakao M., Nomiya H., Shimada K.;  
RT "Structures of human genes coding for cytokine LD78 and their  
expression."  
RL Mol. Cell. Biol. 10:3646-3658(1990).  
RN [5]  
RP SEQUENCE OF 23-92 FROM N.A.  
RA Jang J.S., Kim B.E.;  
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP SEQUENCE OF 24-92, AND MUTAGENESIS OF ASP-49.  
RX MEDLINE=96127782; PubMed=8541527;  
RA Hunter M.G., Bawden L., Brotherton D., Craig S., Cribbes S.,  
RA Czaplowski L.G., Dexter T.M., Drummond A.H., Gearing A.H.,  
RA Heyworth C.M., Lord B.I., Mccourt M., Varley P.G., Wood L.M.,  
RA Edwards R.M., Lewis P.J.;  
RT "BB-10010: an active variant of human macrophage inflammatory protein-  
1 alpha with improved pharmaceutical properties."  
RL Blood 86:4400-4408(1995).  
RN [7]  
RP SEQUENCE OF 27-40 AND 71-83, AND FUNCTION.

Q90826; Q910C9;  
01-NOV-1997 (Rel. 35, Created)  
28-FEB-2003 (Rel. 41, Last sequence update)  
28-FEB-2003 (Rel. 41, Last annotation update)  
Small inducible cytokine A4 homolog precursor (Macrophage inflammatory  
protein 1-beta homolog).  
CCL4 OR SCYA4. (Chicken).  
Gallus gallus (Chicken).  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
Gallus.  
NCBI\_TaxID=9031;  
[1]  
SEQUENCE FROM N.A.  
TISSUE=Bone marrow;  
MEDLINE=95369710; PubMed=7642115;  
Petrenko O., Ischenko I., Enrietto P.J.;  
"Isolation of a cDNA encoding a novel chicken chemokine homologous to  
mammalian macrophage inflammatory protein-1 beta."  
Gene 160:305-306(1995).  
[2]  
SEQUENCE FROM N.A.  
Hughes S.M., Bumstead N.;  
"Mapping of the gene encoding the chicken homologue of the mammalian  
chemokine SCYA4."  
Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
[3]  
SEQUENCE OF 14-90 FROM N.A.  
Petrenko O., Enrietto P.J.;  
Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.  
-!- FUNCTION: MONOKINE WITH INFLAMMATORY AND CHEMOKINETIC PROPERTIES  
(BY SIMILARITY).  
-!- SUBUNIT: Homodimer (By similarity).  
-!- SUBCELLULAR LOCATION: Secreted.  
-!- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE  
C-C) (CHEMOKINE CC).

-----  
This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
modified and this statement is not removed. Usage by and for commercial  
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
EMBL; L34553; AAA48747.1; -;  
EMBL; AJ243034; CAB45103.1; -;  
HSSP; P13236; 1HUM.  
InterPro; IPR000827; CC\_chemokine\_sml.  
InterPro; IPR001811; Chemokine\_IL8.  
Pfam; PF00048; IL8; 1.  
SMART; SM00199; SCY; 1.  
PROSITE; PS00472; SMALL\_CYTOKINES\_CC; 1.  
Cytokine; Chemotaxis; Signal.  
SIGNAL 1 21 BY SIMILARITY.  
CHAIN 22 90 SMALL INDUCIBLE CYTOKINE A4 HOMOLOG.  
DISULFID 32 56 BY SIMILARITY.  
DISULFID 33 72 BY SIMILARITY.  
CONFLICT 87 87 M -> L (IN REF. 1).  
SEQUENCE 90 AA; 9987 MW; 50AF9679A267408F CRC64;  
Query Match 52.6%; Score 251.5; DB 1; Length 90;



MEDLINE=96106406; PubMed=8525373;  
Cocchi F., DeVico A.L., Garzino-Demo A., Arya S.K., Gallo R.C.,  
Lusso P.;  
"Identification of RANTES, MIP-1 alpha, and MIP-1 beta as the major  
HIV-suppressive factors produced by CD8+ T cells.";  
Science 270:1811-1815(1995).  
-!- FUNCTION: MONOKINE WITH INFLAMMATORY AND CHEMOKINETIC PROPERTIES.  
BINDS TO CCR1, CCR4 AND CCR5. ONE OF THE MAJOR HIV-SUPPRESSIVE  
FACTORS PRODUCED BY CD8+ T CELLS. RECOMBINANT MIP-1-ALPHA INDUCES  
A DOSE-DEPENDENT INHIBITION OF DIFFERENT STRAINS OF HIV-1, HIV-2,  
AND SIMIAN IMMUNODEFICIENCY VIRUS (SIV).  
-!- SUBCELLULAR LOCATION: Secreted.  
-!- INDUCTION: BY TPA OR PHA (TPA = 12-O-TETRADECANOYL PHORBOL-13  
ACETATE (TUMOR PROMOTER); PHA = PHYTOHEMAGGLUTININ (T-CELL  
MITOGEN)).  
-!- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE  
C-C) (CHEMOKINE CC). STRONG, TO SCYA3L1.  
-----  
This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
modified and this statement is not removed. Usage by and for commercial  
entities requires a license agreement (See [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/)  
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
EMBL; D00044; BAA00029.1; -;  
EMBL; M23452; AAA36316.1; -;  
EMBL; M25315; AAAS7255.1; -;  
EMBL; X03754; CAA27388.1; -;  
EMBL; X04018; CAA27643.1; ALT\_SEQ.  
EMBL; M23178; AAA35858.1; -;  
EMBL; D90144; BAA14172.1; -;  
EMBL; AF043339; AAC03539.1; -;  
PIR; A35673; A30574.  
PDB; 1B50; 22-JUL-99.  
PDB; 1B53; 22-JUL-99.  
Genew; HGNC:10627; CCL3.  
MIM; 182283; -;  
GO; GO:0005625; C:soluble fraction; TAS.  
GO; GO:0003800; F:antiviral response protein activity; TAS.  
GO; GO:0008009; F:chemokine activity; TAS.  
GO; GO:0004871; F:signal transducer activity; TAS.  
GO; GO:0006961; P:antibacterial humoral response (sensu Inver. . .; TAS.  
GO; GO:0006874; P:calcium ion homeostasis; TAS.  
GO; GO:0006928; P:cell motility; TAS.  
GO; GO:0007267; P:cell-cell signaling; TAS.  
GO; GO:0006935; P:chemotaxis; TAS.  
GO; GO:0006887; P:exocytosis; TAS.  
GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.  
GO; GO:0006955; P:immune response; TAS.  
GO; GO:0006954; P:inflammatory response; TAS.  
GO; GO:0007011; P:regulation of cytoskeleton; TAS.  
GO; GO:0007165; P:signal transduction; TAS.  
GO; GO:0008166; P:viral replication; TAS.  
InterPro; IPR000827; CC chemokine sml.  
InterPro; IPR001811; Chemokine\_IL8.  
Pfam; PF00048; IL8; 1.  
SMART; SM00199; SCY; 1.  
PROSITE; PS00472; SMALL CYTOKINES\_CC; 1.  
Cytokine; Chemotaxis; Inflammatory response; Signal; 3D-structure.  
SIGNAL 1 23  
CHAIN 24 92 SMALL INDUCIBLE CYTOKINE A3.  
DISULFID 33 57 BY SIMILARITY.  
DISULFID 34 73 BY SIMILARITY.  
MUTAGEN 49 49 D->A: IN BB-10010; IMPROVED  
PHARMACEUTICAL PROPERTIES.  
SEQUENCE 92 AA; 10085 MW; 517865D5D6776CA8 CRC64;  
Query Match 51.9%; Score 248; DB 1; Length 92;  
Best Local Similarity 48.4%; Pred. No. 6.5e-21;  
Matches 44; Conservative 22; Mismatches 25; Indels 0; Gaps 0;

QY	1	MKVSARLAVILIATALCAPASAPSYSSDTPCCPAYIARPLPRAHIKEYFYFTSGKCNSP	60
Db	1	MQVSTAALAVLLCTMALCNQFSASLAADPTACCFSYTSRQIPQNFIADYFETSSQCCKP	60
QY	61	AVFEVTRKNRQVCANPEKKWVREYNLSMS	91
Db	61	GVIFLTKRSRQVCADPSEEWVKVSDLELS	91
<b>RESULT 11</b>			
SY03_RAT	SY03_RAT	STANDARD;	PRT; 92 AA.
ID	AC	P50229;	
DT	DT	01-OCT-1996 (Rel. 34, Created)	
DT	DT	01-OCT-1996 (Rel. 34, Last sequence update)	
DT	DT	28-FEB-2003 (Rel. 41, Last annotation update)	
DE	DE	Small inducible cytokine A3 precursor (CCL3) (Macrophage inflammatory protein 1-alpha) (MIP-1-alpha).	
GN	GN	CCL3 OR SCYA3 OR MIP1A.	
OS	OS	Rattus norvegicus (Rat).	
OC	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	OC	Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	
OX	OX	NCBI_TaxID=10116;	
RN	RN	[1]	
RP	RP	SEQUENCE FROM N.A.	
RC	RC	TISSUE=Lung;	
RX	RX	MEDLINE=95298037; PubMed=7779098;	
RA	RA	Shi M.M., Godleski J.J., Paulauskis J.D.;	
RT	RT	"Molecular cloning and posttranscriptional regulation of macrophage inflammatory protein-1 alpha in alveolar macrophages.";	
RL	RL	Biochem. Biophys. Res. Commun. 211:289-295(1995).	
RN	RN	[2]	
RP	RP	SEQUENCE FROM N.A.	
RC	RC	STRAIN=Long Evans; TISSUE=Lung;	
RX	RX	MEDLINE=95238980; PubMed=7722328;	
RA	RA	Shanley T.P., Schmal H., Friedl H.P., Jones M.L., Ward P.A.;	
RT	RT	"Role of macrophage inflammatory protein-1 alpha (MIP-1 alpha) in acute lung injury in rats.";	
RL	RL	J. Immunol. 154:4793-4802(1995).	
RN	RN	[3]	
RP	RP	SEQUENCE OF 24-57.	
RC	RC	STRAIN=Wistar;	
RX	RX	MEDLINE=96183056; PubMed=8607872;	
RA	RA	Nakagawa H., Shiota S., Takano K., Shibata F., Kato H.;	
RT	RT	"Cytokine-induced neutrophil chemoattractant (CINC)-2 alpha, a novel member of rat GRO/CINCS, is a predominant chemokine produced by lipopolysaccharide-stimulated rat macrophages in culture.";	
RL	RL	Biochem. Biophys. Res. Commun. 220:945-948(1996).	
CC	CC	-!- FUNCTION: MONOKINE WITH INFLAMMATORY AND CHEMOKINETIC PROPERTIES. HAS CHEMOTACTIC ACTIVITY FOR MONOCYTES, NEUTROPHILS, EOSINOPHILS, BASOPHILS, AND LYMPHOCYTES. REQUIRED FOR LUNG TNF-ALPHA PRODUCTION, NEUTROPHIL RECRUITMENT AND SUBSEQUENT LUNG INJURY AND MAY FUNCTION AS AN AUTOCRINE MEDIATOR FOR THE MACROPHAGE PRODUCTION OF TNF-ALPHA WHICH IN TURN UP-REGULATES VASCULAR ADHESION MOLECULES REQUIRED FOR NEUTROPHIL INFUX. THIS PROTEIN BINDS HEPARIN.	
CC	CC	-!- SUBCELLULAR LOCATION: Secreted.	
CC	CC	-!- INDUCTION: BY LIPOPOLYSACCHARIDE (LPS).	
CC	CC	-!- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE C-C) (CHEMOKINE CC).	
CC	CC	-----	
CC	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announcement or send an email to license@isb-sib.ch).	
CC	CC	-----	
DR	DR	EMBL; U22414; AAA80608.1; -.	
DR	DR	EMBL; U06435; AAA96498.1; -.	
DR	DR	PIR; I52322; I52322.	
DR	DR	HSSP; P13236; IHUM.	



	EMBL; M23447; AAA40146.1; -
	EMBL; X12531; CAA31047.1; -
	EMBL; X53372; CAA37452.1; -
	EMBL; J04491; AAA40304.1; -
	EMBL; M73061; AAA39707.1; -
	EMBL; AF065939; AAC17506.1; -
	EMBL; AF065940; AAC17507.1; -
	EMBL; AF065941; AAC17508.1; -
	EMBL; AF065942; AAC17509.1; -
	EMBL; AF065943; AAC17510.1; -
	PIR; S11685; A32393.
	HSSP; P13236; LHUM.
	MGI; 98260; Ccl3.
	GO; GO:0008009; F:chemokine activity; IDA.
	InterPro; IPR000827; CC_chemkine_sml.
	InterPro; IPR001811; Chemokine_IL8.
	Pfam; PF00048; IL8; 1.
	SMART; SM00199; SCY; 1.
	PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
KW	Cytokine; Chemotaxis; Inflammatory response; Signal.
FT	SIGNAL 1 23
FT	CHAIN 24 92 SMALL INDUCIBLE CYTOKINE A3.
FT	DISULFID 34 57 BY SIMILARITY.
FT	DISULFID 35 73 BY SIMILARITY.
FT	CONFLICT 22 22 F -> L (IN REF. 3).
FT	CONFLICT 62 62 V -> A (IN REF. 3).
SQ	SEQUENCE 92 AA; 10345 MW; 8BFF2DE7C6DEDD38 CRC64;

Query Match 50.8%; Score 243; DB 1; Length 92;  
 Best Local Similarity 48.9%; Pred. No. 2.3e-20;  
 Matches 45; Conservative 19; Mismatches 26; Indels 2; Gaps 2;

Qy	1 MKVSAARLAVILIATALCAPASAPSYSDT-TPCCFAYIARPLRAHIKEYFYTSKGCSN 59                :  :     ::    :    :    :
Dd	1 MKVSTTALAVALLCMTLTLCNQVFSPAGYADPTACCFYSY-SRKIPRQFIVDYFETSSLCSQ 59    :
Qy	60 PAVVFTRKNRVQCANPEKKVREYINSLEMS 91    :
Dd	60 PGVIFLTRKNRQICADSKETWVQEYITDLELN 91    :

RESULT 14

SY04 HUMAN

ID	SY04 HUMAN	STANDARD;	PRT;	92 AA.
AC	P13236; P22617; Q13704;			
DT	01-JAN-1990 (Rel. 13, Created)			
DT	01-JAN-1990 (Rel. 13, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Small inducible cytokine A4 precursor (CCL4) (Macrophage inflammatory protein 1-beta) (MIP-1-beta) (T-cell activation protein 2) (ACT-2) (PAT 744) (H400) (SIS-gamma) (Lymphocyte activation gene-1 protein) (LAG-1) (HC21) (G-26 T lymphocyte-secreted protein).			
GN	CCL4 OR SCYA4 OR MIP1B OR LAG1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=89071764; PubMed=2462251;			
RA	Lipes M.A., Napolitano M., Jeang K.-T., Chang N.T., Leonard W.J.;			
RT	"Identification, cloning, and characterization of an immune activation gene.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 85:9704-9708(1988).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=89140347; PubMed=2521882;			
RA	Zipfel P.F., Balke J., Irving S.G., Kelly K., Siebenlist U.;			
RT	"Mitogenic activation of human T cells induces two closely related genes which share structural similarities with a new family of secreted factors.";			
RL	J. Immunol. 142:1582-1590(1989).			

[3] SEQUENCE FROM N.A.  
MEDLINE=89093958; PubMed=2521353;  
Brown K.D., Zurawski S.M., Mosmann T.R., Zurawski G.;  
"A family of small inducible proteins secreted by leukocytes are members of a new superfamily that includes leukocyte and fibroblast-derived inflammatory agents, growth factors, and indicators of various activation processes.";  
J. Immunol. 142:679-687(1989).  
[4] SEQUENCE FROM N.A.  
MEDLINE=91061800; PubMed=2247088;  
Baixeras E., Roman-Roman S., Jitsukawa S., Genevee C., Mechiche S., Viegas-Pequignot E., Hercend T., Triebel F.;  
"Cloning and expression of a lymphocyte activation gene (LAG-1).";  
Mol. Immunol. 27:1091-1102(1990).  
[5] SEQUENCE FROM N.A.  
TISSUE=T-cell;  
MEDLINE=89325421; PubMed=2568930;  
Chang H.C., Reinherz E.L.;  
"Isolation and characterization of a cDNA encoding a putative cytokine which is induced by stimulation via the CD2 structure on human T lymphocytes.";  
Eur. J. Immunol. 19:1045-1051(1989).  
[6] SEQUENCE FROM N.A.  
MEDLINE=91373378; PubMed=1894635;  
Napolitano M., Modi W.S., Cevario S.J., Gnarr J.R., Seuanez H.N., Leonard W.J.;  
"The gene encoding the Act-2 cytokine. Genomic structure, HTLV-I/Tax responsiveness of 5' upstream sequences, and chromosomal localization.";  
J. Biol. Chem. 266:17531-17536(1991).  
[7] SEQUENCE FROM N.A.  
Birren B., Fasman K., McKernan K., Nusbaum C., Richardson P., Lander E.;  
Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
[8] SEQUENCE OF 6-92 FROM N.A.  
MEDLINE=90038522; PubMed=2809212;  
Miller M.D., Hata S., Waal Malefyt R., Krangel M.S.;  
"A novel polypeptide secreted by activated human T lymphocytes.";  
J. Immunol. 143:2907-2916(1989).  
[9] RECEPTOR INTERACTION.  
MEDLINE=98180363; PubMed=9521068;  
Bernardini G., Hedrick J., Sozzani S., Luini W., Spinetti G., Weiss M., Menon S., Zlotnik A., Mantovani A., Santoni A., Napolitano M.;  
"Identification of the CC chemokines TARC and macrophage inflammatory protein-1 beta as novel functional ligands for the CCR8 receptor.";  
Eur. J. Immunol. 28:582-588(1998).  
[10] FUNCTION.  
MEDLINE=96106406; PubMed=8525373;  
Cocchi F., DeVico A.L., Garzino-Demo A., Arya S.K., Gallo R.C., Lusso P.;  
"Identification of RANTES, MIP-1 alpha, and MIP-1 beta as the major HIV-suppressive factors produced by CD8+ T cells.";  
Science 270:1811-1815(1995).  
[11] STRUCTURE BY NMR.  
MEDLINE=94182137; PubMed=8134838;  
Lodi P.J., Garrett D.S., Kucewski J., Tsang M.L.S., Weatherbee J.A., Leonard W.J., Gronenborn A.M., Clore G.M.;  
"High-resolution solution structure of the beta chemokine hMIP-1 beta by multidimensional NMR.";  
Science 263:1762-1767(1994).  
-!- FUNCTION: MONOKINE WITH INFLAMMATORY AND CHEMOKINETIC PROPERTIES. BINDS TO CCR5 AND TO CCR8. ONE OF THE MAJOR HIV-SUPPRESSIVE FACTORS PRODUCED BY CD8+ T CELLS. RECOMBINANT MIP-1-BETA INDUCES A

CC DOSE-DEPENDENT INHIBITION OF DIFFERENT STRAINS OF HIV-1, HIV-2, AND SIMIAN IMMUNODEFICIENCY VIRUS (SIV).  
CC -!- SUBUNIT: Homodimer.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- INDUCTION: By mitogens.  
CC -!- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE C-C) (CHEMOKINE CC).  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; M23502; AAA36656.1; -;  
CC EMBL; M25316; AAA57256.1; -;  
CC EMBL; J04130; AAA51576.1; -;  
CC EMBL; X53683; CAA37723.1; -;  
CC EMBL; X53682; CAA37722.2; ALT\_SEQ.  
CC EMBL; X16166; CAA34291.1; -;  
CC EMBL; M6203; AAB00790.1; -;  
CC EMBL; M6201; AAB00790.1; JOINED.  
CC EMBL; M6202; AAB00790.1; JOINED.  
CC EMBL; AC003976; -; NOT ANNOTATED\_CDS.  
CC EMBL; M57503; AAA36752.1; -;  
CC PIR; JH0319; A31767.  
CC PDB; 1HUM; 30-APR-94.  
CC PDB; 1HUN; 30-APR-94.  
CC PDB; 1JE4; 03-OCT-01.  
CC Genew; HGNC:10630; CCL4.  
CC MIM; 182284; -;  
CC GO; GO:0005615; C:extracellular space; TAS.  
CC GO; GO:0008009; F:chemokine activity; TAS.  
CC GO; GO:0004716; F:receptor signaling protein tyrosine kinase . . . ; TAS.  
CC GO; GO:0007155; P:cell adhesion; TAS.  
CC GO; GO:0008151; P:cell growth and/or maintenance; TAS.  
CC GO; GO:0006928; P:cell motility; TAS.  
CC GO; GO:0007267; P:cell-cell signaling; TAS.  
CC GO; GO:0007163; P:establishment and/or maintenance of cell po. . . ; TAS.  
CC GO; GO:0006955; P:immune response; TAS.  
CC GO; GO:0006954; P:inflammatory response; TAS.  
CC GO; GO:0009615; P:response to viruses; TAS.  
CC GO; GO:0007165; P:signal transduction; TAS.  
CC GO; GO:0008166; P:viral replication; TAS.  
CC InterPro; IPR000827; CC\_chemokine\_sml.  
CC InterPro; IPR001811; Chemokine\_IL8.  
CC Pfam; PF00048; IL8; 1.  
CC SMART; SM00199; SCY; 1.  
CC PROSITE; PS00472; SMALL CYTOKINES\_CC; 1.  
KW Cytokine; Chemotaxis; Inflammatory response; Signal; 3D-structure.  
FT SIGNAL 1 23  
FT CHAIN 24 92 SMALL INDUCIBLE CYTOKINE A4.  
FT DISULFID 34 58 BY SIMILARITY.  
FT DISULFID 35 74 BY SIMILARITY.  
FT CONFLICT 6 6 T -> C (IN REF. 7).  
FT CONFLICT 15 15 A -> S (IN REF. 6).  
FT CONFLICT 20 20 P -> L (IN REF. 2).  
FT CONFLICT 40 45 ARKLPR -> REASS (IN REF. 3).  
FT CONFLICT 56 56 S -> I (IN REF. 8).  
FT CONFLICT 70 70 S -> G (IN REF. 6).  
FT CONFLICT 80 80 S -> T (IN REF. 7 AND 8).  
FT STRAND 29 29  
FT STRAND 33 33  
FT HELIX 45 47  
FT STRAND 50 53  
FT STRAND 63 66  
FT STRAND 72 75  
FT TURN 77 78  
FT HELIX 80 92  
SQ SEQUENCE 92 AA; 10212 MW; F2EA7CF341B0E258 CRC64;



Query Match 50.7%; Score 242.5; DB 1; Length 92;  
Best Local Similarity 45.7%; Pred. No. 2.7e-20;  
Matches 42; Conservative 23; Mismatches 26; Indels 1; Gaps 1;  
  
1 MKVSAARLAVILIATALCAPASAPYSSD-TTPCCFAYIARPLPRAHIKEYFYTSGKCSN 59  
||: : : : : ||: : : : : ||: : : : : ||: : : : : ||: : : : : ||  
1 MKLCVTVLSLLMLVAAFCSFALSAPMGSDPPTACCFSTARKLPNRFVVDYETSSLCSSQ 60  
  
60 PAVVFVTRKNRQVCANPEKKWVREYINSLEMS 91  
||||| : : : : : ||: : : : : ||: : : : : ||: : : : : ||: : : : : ||  
61 PAVVFQTKRSKQVCADPSESQVYVYDLELN 92

Search completed: December 16, 2003, 15:38:22  
Job time : 11.4426 secs

RESULT 15  
SY04\_RAT STANDARD; PRT; 92 AA.  
P50230;  
01-OCT-1996 (Rel. 34, Created)  
01-OCT-1996 (Rel. 34, Last sequence update)  
28-FEB-2003 (Rel. 41, Last annotation update)  
Small inducible cytokine A4 precursor (CCL4) (Macrophage inflammatory  
protein 1-beta) (MIP-1-beta).  
CCL4 OR SCYA4 OR MIP1B.  
Rattus norvegicus (Rat).  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
NCBI\_TaxID=10116;  
[1]  
SEQUENCE FROM N.A.  
STRAIN=Long Evans; TISSUE=Lung;  
Jones M.L., Shanley T.P., Schmal H., Friedl H.P., Ward P.A.;  
Submitted (FEB-1994) to the EMBL/GenBank/DBJ databases.  
-!- FUNCTION: MONOKINE WITH INFLAMMATORY AND CHEMOKINETIC PROPERTIES.  
-!- SUBUNIT: Homodimer (By similarity).  
-!- SUBCELLULAR LOCATION: Secreted.  
-!- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE  
C-C) (CHEMOKINE CC).

-----  
This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
modified and this statement is not removed. Usage by and for commercial  
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----

EMBL; U06434; AAA96497.1; -.  
HSSP; P13236; IHUM.  
InterPro; IPR000827; CC\_chemkine\_sml.  
InterPro; IPR001811; Chemokine\_IL8.  
Pfam; PF00048; IL8; 1.  
SMART; SM00199; SCY; 1.  
PROSITE; PS00472; SMALL\_CYTOKINES\_CC; 1.  
Cytokine; Chemotaxis; Inflammatory response; Signal.  
SIGNAL 1 23 BY SIMILARITY.  
CHAIN 24 92 SMALL INDUCIBLE CYTOKINE A4.  
DISULFID 34 58 BY SIMILARITY.  
DISULFID 35 74 BY SIMILARITY.  
SEQUENCE 92 AA; 10234 MW; 60B451EEBC7103D CRC64;

Query Match 47.8%; Score 228.5; DB 1; Length 92;  
Best Local Similarity 42.4%; Pred. No. 9.7e-19;  
Matches 39; Conservative 22; Mismatches 30; Indels 1; Gaps 1;

Y 1 MKVSAARLAVILIATALCAPASAPYSSD-TTPCCFAYIARPLPRAHIKEYFYTSGKCSN 59  
||: : : : : ||: : : : : ||: : : : : ||: : : : : ||: : : : : ||  
b 1 MKLCVSAFSLLLLVAAFCDVSLSAPIGSDPPTSCCFSTSRKIHNFVMDYETSSLCSSQ 60  
  
Y 60 PAVVFVTRKNRQVCANPEKKWVREYINSLEMS 91  
||||| : : : : : ||: : : : : ||: : : : : ||: : : : : ||: : : : : ||  
b 61 PAVVFLTKKGRQICADPSEPWPVNEYVNDLELN 92



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.  
protein - protein search, using sw model  
n on: December 16, 2003, 15:36:20 ; Search time 30.3333 Seconds  
(without alignments)  
774.158 Million cell updates/sec

US-09-920-137A-8  
rfect score: 478  
quence: 1 MKVSAARLAVILIATLALCAP.....VCANPEKKWVREYINSLEMS 91

oring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

arched: 830525 seqs, 258052604 residues  
tal number of hits satisfying chosen parameters: 830525

nimum DB seq length: 0  
ximum DB seq length: 2000000000  
st-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

tabase : SPTREMBL 23: \*  
1: sp\_archaea: \*  
2: sp\_bacteria: \*  
3: sp\_fungi: \*  
4: sp\_human: \*  
5: sp\_invertebrate: \*  
6: sp\_mammal: \*  
7: sp\_mhc: \*  
8: sp\_organelle: \*  
9: sp\_phage: \*  
10: sp\_plant: \*  
11: sp\_rodent: \*  
12: sp\_virus: \*  
13: sp\_vertebrate: \*  
14: sp\_unclassified: \*  
15: sp\_rvirus: \*  
16: sp\_bacteriap: \*  
17: sp\_archaeap: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	DB ID	Description
1	469	98.1	91	6 Q8HYQ1	Q8hyq1 macaca mula
2	406	84.9	91	6 Q8MKD0	Q8mkd0 equus cabal
3	370	77.4	91	6 Q8HYS0	Q8hys0 canis famil
4	362.5	75.8	92	6 Q8SQ40	Q8sq40 felis silve
5	284.5	59.5	91	13 Q8QG57	Q8gg57 gallus gall
6	283	59.2	50	6 Q8HYN5	Q8hyn5 macaca mula
7	268.5	56.2	93	6 Q8SQA6	Q8sqa6 bos taurus
8	252	52.7	92	6 Q8HYQ3	Q8hyq3 macaca mula
9	251.5	52.6	92	6 Q8HYQ2	Q8hyq2 macaca mula
10	248.5	52.0	90	13 Q9PWA6	Q9pwa6 gallus gall
11	247.5	51.8	92	11 Q91ZL0	Q91zl0 sigmodon hi
12	232	48.5	92	11 Q91Z65	Q91z65 sigmodon hi
13	230.5	48.2	92	4 Q8NHW4	Q8nhw4 homo sapien
14	213	44.6	80	4 Q14745	Q14745 homo sapien
15	213	44.6	89	13 Q918E0	Q918e0 gallus gall
16	204	42.7	91	13 Q8QG56	Q8gg56 gallus gall

17	181	37.9	56	6 Q8HYN4	Q8hyn4 macaca mula
18	181	37.9	88	6 Q8HYP8	Q8hyp8 macaca mula
19	178.5	37.3	92	11 Q9QZU2	Q9qzu2 mus musculu
20	177.5	37.1	92	6 Q8MI76	Q8mi76 bos taurus
21	172.5	36.1	92	11 Q91ZH5	Q91zh5 rattus norv
22	171.5	35.9	81	11 Q9QZU1	Q9qzu1 rattus norv
23	161	33.7	97	6 Q8HXZ5	Q8hxz5 macaca mula
24	155	32.4	100	6 Q9TTQ4	Q9ttq4 equus cabal
25	154	32.2	95	12 Q98158	Q98158 kaposi's sa
26	153.5	32.1	150	11 Q8CGM5	Q8cgm5 sigmodon hi
27	153	32.0	97	6 Q8MIT7	Q8mit7 macaca mula
28	153	32.0	99	6 Q8HYQ0	Q8hyq0 macaca mula
29	151.5	31.7	97	6 Q9TTS6	Q9tts6 bos taurus
30	151	31.6	99	6 Q8MKC8	Q8mkc8 equus cabal
31	150	31.4	49	6 Q8HYN3	Q8hyn3 macaca mula
32	150	31.4	100	6 Q95MD5	Q95md5 bos taurus
33	149	31.2	99	6 Q9TTQ3	Q9ttq3 equus cabal
34	145.5	30.4	148	11 Q9QYD7	Q9qyd7 mus musculu
35	140.5	29.4	120	6 Q8HYP4	Q8hyp4 macaca mula
36	138	28.9	81	6 Q9TTQ2	Q9ttq2 equus cabal
37	138	28.9	91	13 Q8JIM5	Q8jim5 paralichthy
38	136	28.5	91	13 Q8AV56	Q8av56 paralichthy
39	134	28.0	91	13 Q8JIM4	Q8jim4 paralichthy
40	131.5	27.5	101	12 Q8JRS7	Q8jrs7 guinea pig
41	130	27.2	32	4 Q9UBG2	Q9ubg2 homo sapien
42	130	27.2	98	6 Q8HYP7	Q8hyp7 macaca mula
43	128.5	26.9	94	6 Q8HYP9	Q8hyp9 macaca mula
44	127	26.6	95	13 Q8AYB2	Q8ayb2 ictalurus p
45	126.5	26.5	119	11 Q8K477	Q8k477 rattus norv

ALIGNMENTS

RESULT 1  
Q8HYQ1  
ID Q8HYQ1 PRELIMINARY; PRT; 91 AA.  
AC Q8HYQ1;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Chemokine CCL5/RANTES.  
OS Macaca mulatta (Rhesus macaque).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;  
OC Cercopitheciniae; Macaca.  
OX NCBI\_TaxID=9544;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Basu S., Schaefer T.M., Ghosh M., Fuller C.L., Reinhart T.A.;  
RT "Comprehensive cloning and sequencing reveals evolutionary  
RT conservation among all groups of rhesus macaque chemokines."  
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF449268; AAN76072.1; -.  
SQ SEQUENCE 91 AA; 10019 MW; BCBDE69ED0573803B CRC64;

Query Match 98.1%; Score 469; DB 6; Length 91;  
Best local Similarity 96.7%; Pred. No. 1.7e-47;  
Matches 88; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKVSAARLAVILIATLALCAPASAPSYSSDTPCCFAYIARPLPRAHIKEYFYTSKGKCSNP 60  
Db 1 MKVSAARLAVILVATLALCAPASASPHASDTPCCFAYIARPLPRAHIKEYFYTSKGKCSNP 60  
QY 61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91  
Db 61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91

RESULT 2  
Q8MKD0  
ID Q8MKD0 PRELIMINARY; PRT; 91 AA.  
AC Q8MKD0;

01-OCT-2002 (TrEMBLrel. 22, Created)  
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
Small inducible cytokine A5 RANTES.  
Equus caballus (Horse).  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
NCBI\_TaxID=9796;  
[1]  
SEQUENCE FROM N.A.  
Takafuji V.A., Sharova L.V., Crisman M.V., Howard R.D.;  
"Equus caballus RANTES mRNA";  
Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
EMBL; AF506970; AAM34212.1; -  
InterPro; IPR000827; CC\_chemkine\_sml.  
InterPro; IPR001811; Chemokine\_IL8.  
Pfam; PF00048; IL8; 1.  
SMART; SM00199; SCY; 1.  
PROSITE; PS00472; SMALL\_CYTOKINES\_CC; 1.  
SEQUENCE 91 AA; 10159 MW; AEB253E8CD4ED7FD CRC64;  
  
Query Match 84.9%; Score 406; DB 6; Length 91;  
Best Local Similarity 83.5%; Pred. No. 4.2e-40;  
Matches 76; Conservative 4; Mismatches 11; Indels 0; Gaps 0;  
  
1 MKVSAARLAVILIATATLALCAPASAPSYSSDTPCCFAYIARPLPRAHIKEYFYTSGKCSNP 60  
|||||  
1 MKVFAAALAVILATATCTPASPASPYASDTPCCFAYISRPLPRAHIQYFYTSSKCSIP 60  
|||||  
61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91  
|||||  
61 AVVFVTRKQVCANPEKKWVREYINSLEMS 91  
  
RESULT 3  
Q8HYSO PRELIMINARY; PRT; 91 AA.  
Q8HYSO;  
01-MAR-2003 (TrEMBLrel. 23, Created)  
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
RANTES protein.  
RANTES.  
Canis familiaris (Dog).  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
NCBI\_TaxID=9615;  
[1]  
SEQUENCE FROM N.A.  
Enomoto A., Kano R., Hasegawa A.;  
"molecular cloning of canine RANTES gene";  
Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.  
EMBL; AB098562; BAC53725.1; -  
SEQUENCE 91 AA; 10179 MW; 01D79538CB8148E7 CRC64;  
  
Query Match 77.4%; Score 370; DB 6; Length 91;  
Best Local Similarity 75.8%; Pred. No. 7.1e-36;  
Matches 69; Conservative 8; Mismatches 14; Indels 0; Gaps 0;  
  
1 MKVSAARLAVILIATATLALCAPASAPSYSSDTPCCFAYIARPLPRAHIKEYFYTSGKCSNP 60  
|||||  
1 MKVSAATFAILLATATFRAPASAPSYASDTPCCFAYISGRPLPFTHVQYFYTSSKCSMP 60  
|||||  
61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91  
|||||  
61 AVVFVTRKQVCANPEKKWVREYINSLEMS 91  
  
RESULT 4  
Q8SQ40 PRELIMINARY; PRT; 92 AA.  
Q8SQ40;  
01-JUN-2002 (TrEMBLrel. 21, Created)

DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE RANTES protein.  
GN RANTES.  
OS Felis silvestris catus (Cat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
OX NCBI\_TaxID=9685;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Kimura T., Kano R., Hasegawa A.;  
RT "molecular cloning of feline RANTES gene";  
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB083479; BAB88940.1; -  
DR InterPro; IPR000827; CC\_chemkine\_sml.  
DR InterPro; IPR001811; Chemokine\_IL8.  
DR Pfam; PF00048; IL8; 1.  
DR SMART; SM00199; SCY; 1.  
DR PROSITE; PS00472; SMALL\_CYTOKINES\_CC; 1.  
SQ SEQUENCE 92 AA; 10167 MW; 2E6F087140BA3CE8 CRC64;  
  
Query Match 75.8%; Score 362.5; DB 6; Length 92;  
Best Local Similarity 72.8%; Pred. No. 5.5e-35;  
Matches 67; Conservative 10; Mismatches 14; Indels 1; Gaps 1;  
  
QY 1 MKVSAARLAVILIATATLALCAPASAPSYSSDTPCCFAYIARPLPRAHIKEYFYTSGKCSNP 60  
|||||  
Db 1 MKVSTAFAVLTLTAAAFCTPASASPYASDTPCCFAYLSHPLPLTHLQYFYTSSKCSMP 60  
|||||  
QY 61 AVVFVTRKNRQVCANPEKKWVREY-INSLEMS 91  
|||||  
Db 61 AVVFVTRRKRQVCANPQKKWVRDKGINSLEMN 92  
  
RESULT 5  
Q8QG57 PRELIMINARY; PRT; 91 AA.  
Q8QG57;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Chemokine ah294.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21655115; PubMed=11797102;  
RA Hughes S., Haynes A., O'Regan M., Bumstead N.;  
RT "Identification, mapping, and phylogenetic analysis of three novel  
RT chicken CC chemokines";  
RL Immunogenetics 53:674-683(2001).  
DR EMBL; AY037859; AAK84432.1; -  
DR InterPro; IPR000827; CC\_chemkine\_sml.  
DR InterPro; IPR001811; Chemokine\_IL8.  
DR Pfam; PF00048; IL8; 1.  
DR SMART; SM00199; SCY; 1.  
DR PROSITE; PS00472; SMALL\_CYTOKINES\_CC; 1.  
SQ SEQUENCE 91 AA; 10154 MW; 744A64BB229194EF CRC64;  
  
Query Match 59.5%; Score 284.5; DB 13; Length 91;  
Best Local Similarity 57.8%; Pred. No. 7.9e-26;  
Matches 52; Conservative 15; Mismatches 22; Indels 1; Gaps 1;  
  
QY 1 MKVSAARLAVILIATATLALCAPASAPSYSSDTPCCFAYIARPLPRAHIKEYFYTSGKCSNP 60  
|||||  
Db 2 MTAVAVSLSILLVA-ALFPQASSSPFGADTTVCFFNYSVRKLPQNHVKDYFYTSSKCPQA 60  
|||||  
QY 61 AVVFVTRKNRQVCANPEKKWVREYINSLEM 90  
|||||  
Db 61 AVVFITRKRQVCANPDARWVKEYINFLEL 90



```

>ULT 10
>WA6
Q9PWA6 PRELIMINARY; PRT; 90 AA.
Q9PWA6;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Chemokine.
SCYA4.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
NCBI_TaxID=9031;
[1]
SEQUENCE FROM N.A.
Hughes S.M., Bumstead N.;
"Mapping of the gene encoding the chicken homologue of the mammalian
chemokine SCYA4."
Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
EMBL; AF146730; AAD48772.1; -.
HSSP; P13236; IHUM.
InterPro; IPR000827; CC_chemkine_sml.
InterPro; IPR001811; Chemokine_IL8.
Pfam; PF00048; IL8; 1.
SMART; SM00199; SCY; 1.
PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
SEQUENCE 90 AA; 9986 MW; 50AF9679A26751CB CRC64;

Query Match 52.0%; Score 248.5; DB 13; Length 90;
Best Local Similarity 50.0%; Pred. No. 1.3e-21;
Matches 46; Conservative 20; Mismatches 23; Indels 3; Gaps 2;

1 MKVSAARLAVILIATATCAPASASPYSSD-TTPCCFAYIARPLPRAHIKEYFTSGKCSN 59
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1 MKVSVAAALAVLLI--AICYQTSAAPVGSDDPTSCCFTYISRLPFSFVADYYETNSQCPH 58

60 PAVVFVTRKNRQVCANPEKKWVREYINSLEMS 91
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
59 AGVVFITRKGREVCANPQNDWVQDYMNMKMLN 90

SULT 11
1ZLO
Q91ZLO PRELIMINARY; PRT; 92 AA.
Q91ZLO;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Macrophage inflammatory protein 1 beta.
MIP-1BETA.
Sigmodon hispidus (Hispid cotton rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
Sigmodon.
NCBI_TaxID=42415;
[1]
SEQUENCE FROM N.A.
Blanco J.C., Pletneva L.M., Prince G.A.;
"Sigmodon hispidus cytokines, chemokines and interferons."
Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
EMBL; AF421392; AAL16933.1; -.
HSSP; Q9Y258; 1G2S.
InterPro; IPR000827; CC_chemkine_sml.
InterPro; IPR001811; Chemokine_IL8.
Pfam; PF00048; IL8; 1.
SMART; SM00199; SCY; 1.
PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
SEQUENCE 92 AA; 10195 MW; A34FDE21E6FA9C2E CRC64;

Query Match 51.8%; Score 247.5; DB 11; Length 92;
Best Local Similarity 46.7%; Pred. No. 1.8e-21;
Matches 43; Conservative 21; Mismatches 27; Indels 1; Gaps 1;

1 MKVSAARLAVILIATATCAPASASPYSSD-TTPCCFAYIARPLPRAHIKEYFTSGKCSN 59
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1 MKVPTAVLAVLLCIITLCNQVFSAPYGADTPTFCFSY-GRQIPRKFIADYFQTSSLCSE 59

60 PAVVFVTRKNRQVCANPEKKWVREYINSLEMS 91
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
59 AGVVFITRKGREVCANPQNDWVQDYMNMKMLN 90

SULT 12
Q91Z65 PRELIMINARY; PRT; 92 AA.
Q91Z65;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Macrophage inflammatory protein-1 alpha.
MIP1 ALPHA.
Sigmodon hispidus (Hispid cotton rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
Sigmodon.
NCBI_TaxID=42415;
[1]
SEQUENCE FROM N.A.
Blanco J.C., Pletneva L.M., Prince G.A.;
"Sigmodon hispidus cytokines, chemokines and interferons."
Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
EMBL; AY059407; AAL26704.1; -.
HSSP; Q9Y258; 1G2S.
InterPro; IPR000827; CC_chemkine_sml.
InterPro; IPR001811; Chemokine_IL8.
Pfam; PF00048; IL8; 1.
SMART; SM00199; SCY; 1.
PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
SEQUENCE 92 AA; 10334 MW; CF9AAB3D94DAF79 CRC64;

Query Match 48.5%; Score 232; DB 11; Length 92;
Best Local Similarity 47.8%; Pred. No. 1.2e-19;
Matches 44; Conservative 18; Mismatches 28; Indels 2; Gaps 2;

1 MKVSAARLAVILIATATCAPASASPYSSD-TTPCCFAYIARPLPRAHIKEYFTSGKCSN 59
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1 MKVPTAVLAVLLCIITLCNQVFSAPYGADTPTFCFSY-GRQIPRKFIADYFQTSSLCSE 59

60 PAVVFVTRKNRQVCANPEKKWVREYINSLEMS 91
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
60 PGIIFLTNRHRVCAADPKETWVQEIITDLELN 91

SULT 13
Q8NHW4 PRELIMINARY; PRT; 92 AA.
Q8NHW4;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Macrophage inflammatory protein-1b2.
CCL4L1.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
Nibbs R.J., Barcellos L.F., Townson J.R.;
"Variation in gene copy number of the human chemokines macrophage
inflammatory protein-1a/CCL3 and macrophage inflammatory protein-
1b/CCL4."
Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
EMBL; AY079147; AAL87008.1; -.
InterPro; IPR000827; CC_chemkine_sml.
```





GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

protein - protein search, using sw model

on: December 16, 2003, 15:36:19 ; Search time 36.3005 Seconds  
(without alignments)  
397.904 Million cell updates/sec

le: US-09-920-137A-8  
fect score: 478  
uence: 1 MKVSAARLAVILIATLALCAP.....VCANPEKKWVREYINSLEMS 91

ring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

rchd: 1107863 seqs, 158726573 residues

al number of hits satisfying chosen parameters: 1107863

imum DB seq length: 0  
imum DB seq length: 2000000000

t-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

abase : A\_Geneseq\_19Jun03:\*  
1: /SIDS17/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT.\*  
2: /SIDS17/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT.\*  
3: /SIDS17/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT.\*  
4: /SIDS17/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT.\*  
5: /SIDS17/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT.\*  
6: /SIDS17/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT.\*  
7: /SIDS17/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT.\*  
8: /SIDS17/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT.\*  
9: /SIDS17/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT.\*  
10: /SIDS17/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT.\*  
11: /SIDS17/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT.\*  
12: /SIDS17/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT.\*  
13: /SIDS17/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT.\*  
14: /SIDS17/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT.\*  
15: /SIDS17/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT.\*  
16: /SIDS17/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT.\*  
17: /SIDS17/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT.\*  
18: /SIDS17/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT.\*  
19: /SIDS17/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT.\*  
20: /SIDS17/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT.\*  
21: /SIDS17/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT.\*  
22: /SIDS17/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT.\*  
23: /SIDS17/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT.\*  
24: /SIDS17/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ult No.	Score	Query Match	Length	ID	Description
1	478	100.0	91	AA70802	RANTES protein. H
2	478	100.0	91	AA707665	RANTES. Homo sapi
3	478	100.0	91	AA705299	C-C chemokine, RAN
4	478	100.0	91	AA707235	Wild type RANTES p
5	478	100.0	91	AA707231	Wild type RANTES p
6	478	100.0	91	AA706727	Amino acid sequenc
7	478	100.0	91	AA705790	Human chemokine RA
8	478	100.0	445	AA701766	Novel human secret
9	472	98.7	91	AA704003	Human EST encoded

10	472	98.7	91	23	ABB80929	Human RANTES prote
11	472	98.7	91	23	AAO21079	Wild type RANTES p
12	472	98.7	91	23	AA52443	HIV_Nef1 fusion pr
13	466	97.5	91	23	AAO21086	Protein of R44A-RA
14	466	97.5	91	23	AAO21087	Protein of K68A-RA
15	466	97.5	91	23	AAO21088	Protein of R70A-RA
16	466	97.5	91	23	AAO21089	Protein of K78A-RA
17	466	97.5	91	23	AAO21091	Protein of R82A-RA
18	460.5	96.3	90	20	AAW82720	Human S1SD protein
19	454	95.0	91	23	AAO21081	Protein of triple
20	454	95.0	91	23	AAO21084	Protein of triple
21	451.5	94.5	90	23	AAO21090	Protein of K79A-RA
22	443.5	92.8	92	23	AAO21085	Protein of triple
23	397	83.1	91	23	AAW52444	HIV_Nef1 fusion pr
24	393	82.2	472	22	AAW61799	Chimeric chemokine
25	374	78.2	68	19	AAW29538	RANTES peptide. H
26	374	78.2	68	20	AAW06728	Amino acid fragmen
27	374	78.2	68	20	AAW06760	SDF-1 alpha/RANTES
28	374	78.2	68	20	AAW99707	RANTES sequence.
29	374	78.2	68	21	AAW88331	Human rantes amino
30	374	78.2	68	21	AAW83898	Human RANTES prote
31	374	78.2	68	21	AAW69039	Amino acid sequenc
32	374	78.2	68	23	AAO21100	RANTES chemokine p
33	374	78.2	68	23	AAO20007	Human chemokine ra
34	374	78.2	68	23	AAO14140	Human RANTES prote
35	374	78.2	69	17	AAW97666	Met-RANTES. Synth
36	374	78.2	69	17	AAW97667	Leu-RANTES. Synth
37	374	78.2	69	17	AAW97668	Gln-RANTES. Synth
38	374	78.2	73	19	AAW61765	hRANTES wild-type
39	374	78.2	414	23	AAE22194	RANTES-truncated P
40	370	77.4	67	23	AAO20394	NNY-RANTES analogu
41	370	77.4	67	23	AAO20396	NNY-RANTES analogu
42	370	77.4	67	23	AAO20400	NNY-RANTES analogu
43	370	77.4	67	23	AAO20401	NNY-RANTES analogu
44	370	77.4	69	23	AAU99754	Synthetic erythrop
45	370	77.4	69	23	AAU99773	Polymer modified R

ALIGNMENTS

RESULT 1

AA70802  
ID AA70802 standard; Protein; 91 AA.

XX AA70802;

DT 25-MAR-2003 (updated)  
DT 29-AUG-1995 (first entry)

XX RANTES protein.

KW RANTES; T-cell; T-lymphocyte; heparanase; heparin; heparan sulfate;  
KW arthritis; restenosis; cancer; wound healing.

XX Homo sapiens.

XX WO9504158-A1.

XX 09-FEB-1995.

XX 26-JUL-1994; 94WO-US08207.

XX 29-JUL-1993; 93US-0099866.

XX 13-OCT-1993; 93US-0136117.

XX (UPJO ) UPJOHN CO.

XX Hoogerwerf AJ, Ledbetter SR;

XX WPI; 1995-082239/11.

XX N-PSDB; AAQ85372.

Screening for cpds. with anti-heparanase activity - by detecting inhibition of heparin or heparan sulphate degradation, potentially useful for treating arthritis, restenosis, cancer.

Claim 13; Page 51; 60pp; English.

Purified heparanases, prepared under reducing conditions and activated with transglutaminase, are given in AAR70786-802. Most are prepared by reverse transcription of mRNA from activated human leukocytes, then cloning of the cDNA into pVL1392 baculovirus vector, and expression in Sf9 cells in the presence of reduced glutathione and dithiothreitol.  
(Updated on 25-MAR-2003 to correct PN field.)

Sequence 91 AA;  
Query Match 100.0%; Score 478; DB 16; Length 91;  
Best Local Similarity 100.0%; Pred. No. 3.1e-46;  
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 MKVSAARLAVILIATATCAPASASPYSSDTPCCFAYIARPLPRAHIKEYFYTSKGKCSNP 60  
1 MKVSAARLAVILIATATCAPASASPYSSDTPCCFAYIARPLPRAHIKEYFYTSKGKCSNP 60  
61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91  
61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91

ULT 2  
97665  
AAR97665 standard; Protein; 91 AA.

AAR97665;

14-FEB-1997 (first entry)

RANTES.

Human; RANTES; Raised on Activation, normal T cell derived and Secreted; bone marrow; antagonist; MIP-1alpha; asthma; allergic rhinitis; atopic dermatitis; atheroma; atherosclerosis; rheumatoid arthritis; inflammation; chemotaxis.

Homo sapiens.

Key Location/Qualifiers  
Peptide 1..23 /note= "Signal peptide"  
Protein 24..91 /note= "RANTES, claim 3"

WO9617935-A2.

13-JUN-1996.

07-DEC-1995; 95WO-GB02861.

16-JUN-1995; 95GB-0012319.  
08-DEC-1994; 94GB-0024835.

(GLAX ) GLAXO GROUP LTD.

Proudfoot AEI, Wells TNC;

WPI; 1996-287180/29.  
N-PSDB; AAT30329.

Polypeptide functioning as antagonist to RANTES or to MIP-1-alpha - used in the treatment of e.g. asthma, allergic rhinitis, atheroma/atherosclerosis or rheumatoid arthritis

Example; Fig 1; 33pp; English.

XX This sequence represents full length human RANTES (Raised on Activation, normal T cell derived and Secreted). The DNA encoding this sequence was cloned from a human bone marrow lambda gt11 cDNA library using the primer sequences given in AAT30330-33. RANTES was used in the design of peptides which act as antagonists to RANTES or to MIP-1alpha (see also AAR97666-68). These peptides may be used in the treatment of asthma, allergic rhinitis, atopic dermatitis, atheroma/atherosclerosis or rheumatoid arthritis by inhibiting or reducing inflammation mediated by RANTES or MIP-1alpha. They are also useful in studying RANTES induced chemotaxis, mobilisation of Ca2+ and receptor binding.

XX Sequence 91 AA;

Query Match 100.0%; Score 478; DB 17; Length 91;  
Best Local Similarity 100.0%; Pred. No. 3.1e-46;  
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKVSAARLAVILIATATCAPASASPYSSDTPCCFAYIARPLPRAHIKEYFYTSKGKCSNP 60  
Db 1 MKVSAARLAVILIATATCAPASASPYSSDTPCCFAYIARPLPRAHIKEYFYTSKGKCSNP 60  
QY 61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91  
Db 61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91

RESULT 3

AAY05299  
ID AAY05299 standard; protein; 91 AA.

XX AC AAY05299;

XX DT 25-JUN-1999 (first entry)

XX DE C-C chemokine, RANTES.

XX C-C chemokine; RANTES; MCP2; chemokine antagonist; inflammatory disease; HIV infection; tumour; angiogenesis-related disease; autoimmune disease; haematopoiesis-related disease; CD26/DPP IV; immune disease; diagnosis; atherosclerosis; pulmonary disease; skin disorder; therapy.

XX Homo sapiens.

XX PN EP905240-A1.

XX PD 31-MAR-1999.

XX PF 19-DEC-1997; 97EP-0122471.

XX PR 29-SEP-1997; 97EP-0116863.

XX PA (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.

XX PI Proost P, Struyf S, Van Damme J;

XX DR WPI; 1999-216695/19.

XX PT New amino-terminally truncated C-C chemokines have antagonistic activity, for treatment of immune, inflammatory and infectious diseases

XX PS Claim 5; Fig 1; 30pp; English.

XX This sequence represents the C-C chemokine RANTES. The invention relates to amino-terminally truncated C-C chemokines, having chemokine antagonistic activity. The truncated chemokines are specifically residues 26 to 91 of the RANTES sequence (this sequence) or residues 29 to 99 of the MCP2 sequence (see AAY05300). The new chemokines are useful as medicaments, for diagnosis and/or treatment of diseases which require antagonistic activity of a chemokine e.g. inflammatory diseases, HIV infection, tumours, and angiogenesis- and haematopoiesis-related diseases. The invention also relates to the use of CD26/DPP IV for

Matches	91;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
---------	-----	--------------	----	------------	----	--------	----	------	----

61 AWVETBKNPOVCANPEKKWREYINSTEMS 91



RESULT 6  
AY06727  
AA06727 standard; protein; 91 AA.  
AA06727;  
18-JUN-1999 (first entry)  
Amino acid sequence of native RANTES.

Chemokine; cross-over protein; pharmaceutical; inflammatory; AIDS; viral;  
infectious disease; hematopoiesis; chemoprotection; asthma; RANTES; VMIP;  
allergic rhinitis; atopic dermatitis; rheumatoid arthritis; SDF-1; MPAV;  
stromal cell derived factor 1; Macrophage Inflammatory protein.

Homo sapiens.  
WO9911655-A1.  
11-MAR-1999.  
31-AUG-1998; 98WO-US18096.  
04-SEP-1997; 97US-0057620.  
(GRYP-) GRYPHON SCI.  
Kent SBH, Siani MA, Simon R, Wilken J;  
WPI; 1999-205128/17.

New cross-over proteins for treatment of inflammation and infections  
e.g. AIDS - prepared by ligation of two functional protein modules  
derived from two different parent molecules

Example 4; Page 41; 75pp; English.

The invention relates to a cross-over protein produced by chemical  
ligation of at least two functional protein modules derived from at least  
two parent protein molecules. The cross-over proteins can be used in  
pharmaceutical compositions for therapy of inflammatory and infectious  
diseases including AIDS, and for indications of hematopoiesis and  
chemoprotection. They are also useful for treatment of asthma, allergic  
rhinitis, atopic dermatitis and rheumatoid arthritis. A library  
comprising a collection of cross-over proteins is useful for screening  
for cross-over proteins that are receptor ligands. The libraries comprise  
functionally diverse compounds therefore improving the drug discovery  
process. The proteins and libraries are exemplified by the preparation  
of cross-over chemokines comprising various combinations of peptide  
segments derived from RANTES, SDF-1 (stromal cell derived factor 1), VMIP  
(viral Macrophage Inflammatory protein) and other such chemokines. The  
present sequence represents a native amino acid fragment of RANTES.

Query Match 100.0%; Score 478; DB 20; Length 91;  
Best Local Similarity 100.0%; Pred. No. 3.1e-46;  
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 MKVSAARLAVILIALTALCAPASAPYSSDTTPCCFAYIARPLPRAHIKEYFTSGKCSNP 60  
1 MKVSAARLAVILIALTALCAPASAPYSSDTTPCCFAYIARPLPRAHIKEYFTSGKCSNP 60  
61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91  
61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91

RESULT 7  
AB15790  
D AAB15790 standard; Protein; 91 AA.  
X  
C AAB15790;

17-JAN-2001 (first entry)  
Human chemokine RANTES SEQ ID NO: 21.  
Macrophage recruitment; chemokine derivative; MCP-1; osteoporosis;  
monocyte chemoattractant protein-1; inflammation; atherosclerosis; HIV;  
AIDS; stroke; psoriasis; autoimmune disease; hypertension; endotoxaemia;  
basophil-mediated disease; myocardial infarction; acute ischaemia;  
rheumatoid arthritis; contraception.

Homo sapiens.  
WO200042071-A2.  
20-JUL-2000.  
12-JAN-2000; 2000WO-US00821.  
12-JAN-1999; 99US-0229071.  
17-MAR-1999; 99US-0271192.  
01-DEC-1999; 99US-0452406.  
(NEOR-) NEORX CORP.

Grainger DJ, Tatalick LM;  
WPI; 2000-499101/44.  
N-PSDB; AAA74884.

New peptide 3, amide and heterocyclic compounds and saccharide  
conjugates used for inhibiting chemokine induced activity and for  
treating e.g. stroke, vascular diseases, autoimmune diseases and tumour  
growth

Example 1; Page 134; 387pp; English.

The present invention concerns the identification of a number of  
chemokines which can be used to produce derivatives, agonists and  
antagonists which are then useful in disease treatment. The chemokines  
include sequences AAB15785-B15794, AAB15803-B15813 and AAB15831-B15848.  
These chemokine derivatives can be used to treat diseases such as  
autoimmune diseases, atherosclerosis, osteoporosis, HIV infection and  
AIDS, psoriasis, inflammatory diseases, hypertension, basophil-mediated  
diseases, endotoxaemia, myocardial infarction, acute ischaemia and  
rheumatoid arthritis, and can be used to prevent strokes and as  
contraceptives. The coding sequences for the chemokines can be used in  
gene therapy for the same diseases, as well as in the production of  
animal models.

Sequence 91 AA;

Query Match 100.0%; Score 478; DB 21; Length 91;  
Best Local Similarity 100.0%; Pred. No. 3.1e-46;  
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKVSAARLAVILIALTALCAPASAPYSSDTTPCCFAYIARPLPRAHIKEYFTSGKCSNP 60  
1 MKVSAARLAVILIALTALCAPASAPYSSDTTPCCFAYIARPLPRAHIKEYFTSGKCSNP 60  
61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91  
61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91

RESULT 8  
AAU31766  
ID AAU31766 standard; Protein; 445 AA.  
XX  
AC AAU31766;  
XX  
DT 18-DEC-2001 (first entry)  
XX

Novel human secreted protein #2257.  
Human; vaccination; gene therapy; nutritional supplement;  
stem cell proliferation; haematopoiesis; nerve tissue regeneration;  
immune suppression; immune stimulation; anti-inflammatory; leukaemia.  
Homo sapiens.  
WO200179449-A2.  
25-OCT-2001.  
16-APR-2001; 2001WO-US08656.  
18-APR-2000; 2000US-0552929.  
26-JAN-2001; 2001US-0770160.  
(HYSE-) HYSEQ INC.  
Tang YT, Liu C, Drmanac RT;  
WPI; 2001-611725/70.  
Nucleic acids encoding a range of human polypeptides, useful in genetic  
vaccination, testing and therapy -  
Claim 20; Page 506; 765pp; English.  
The invention relates to novel human secreted polypeptides. The  
polypeptides and antibodies to the polypeptides are useful for  
determining the presence of or predisposition to a disease associated  
with altered levels of polypeptide. The polypeptides are also useful for  
identifying agents (agonists and antagonists) that bind to them. Cells  
expressing the proteins are useful for identifying a therapeutic agent  
for use in treatment of a pathology related to aberrant expression or  
physiological interactions of the polypeptide. Vectors comprising  
the nucleic acids encoding the polypeptides and cells genetically  
engineered to express them are also useful for producing the proteins.  
The proteins are useful in genetic vaccination, testing and  
therapy, and can be used as nutritional supplements. They may be used to  
increase stem cell proliferation; to regulate haematopoiesis; and in  
bone, cartilage, tendon and/or nerve tissue growth or regeneration;  
immune suppression and/or stimulation; as anti-inflammatory agents; and  
in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid  
sequences of novel human secreted proteins of the invention.

Sequence 445 AA;  
Query Match 100.0%; Score 478; DB 22; Length 445;  
Best Local Similarity 100.0%; Pred. No. 1.9e-45;  
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 MKVSAARLAVILIATLALCAPASAPSYSSDTPCCFAYIARPLPRAHIKEYFYTSGKCSNP 60  
|||||  
1 MKVSAARLAVILIATLALCAPASAPSYSSDTPCCFAYIARPLPRAHIKEYFYTSGKCSNP 60  
61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91  
61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91

MULT 9  
124003  
AAM24003 standard; Protein; 91 AA.  
AAM24003;  
12-OCT-2001 (first entry)  
Human EST encoded protein SEQ ID NO: 1528.  
Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;  
tomato; monkey; dog; sea urchin; expressed sequence tag; EST;

KW diagnostics; forensic test; gene mapping; genetic disorder;  
KW biodiversity; gene therapy; nutrition.  
XX Homo sapiens.  
OS WO200154477-A2.  
PN 02-AUG-2001.  
XX 25-JAN-2001; 2001WO-US02687.  
XX 25-JAN-2000; 2000US-0491404.  
PR 17-JUL-2000; 2000US-0617746.  
PR 03-AUG-2000; 2000US-0631451.  
PR 15-SEP-2000; 2000US-0663870.  
XX (HYSE-) HYSEQ INC.  
XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;  
PI Cao Y, Drmanac RA, Zhang J, Werhman T;  
XX WPI; 2001-476164/51.  
DR N-PSDB; AAH98662.  
DR Isolated polypeptide for treatment of diseases, diagnostics, raising  
XX antibodies and research use -  
PT Claim 20; Page 1053; 1275pp; English.  
XX The present invention provides the protein and coding sequences of novel  
CC proteins from a variety of organisms, including human, dog, cat, horse,  
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea  
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)  
CC from the organism of interest. They can be used in diagnostics,  
CC forensics, gene mapping, identification of mutations, to assess  
CC biodiversity and for nutritional purposes. The present sequence is a  
CC protein of the invention.  
XX SQ Sequence 91 AA;

Query Match 98.7%; Score 472; DB 22; Length 91;  
Best Local Similarity 98.9%; Pred. No. 1.5e-45;  
Matches 90; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MKVSAARLAVILIATLALCAPASAPSYSSDTPCCFAYIARPLPRAHIKEYFYTSGKCSNP 60  
|||||  
Db 1 MKVSAARLAVILIATLALCAPASAPSYSSDTPCCFAYIARPLPRAHIKEYFYTSGKCSNP 60  
QY 61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91  
|||||  
Db 61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91

RESULT 10  
ABB80929  
ID ABB80929 standard; Protein; 91 AA.  
XX ABB80929;  
AC ABB80929;  
XX 08-OCT-2002 (first entry)  
DT Human RANTES protein sequence.  
XX Paramyxovirus; infection; RANTES; chemokine; antiviral; CCR1; CCR5;  
KW apoptosis; human.  
XX Homo sapiens.  
OS Key Location/Qualifiers  
XX Peptide 1..23 /note= "signal peptide"  
FT Protein 24..91  
FT /note= "specifically claimed mature protein"

WO200255019-A2.  
18-JUL-2002.  
23-OCT-2001; 2001WO-US45244.  
24-OCT-2000; 2000US-243264P.  
(UNIW ) UNIV WASHINGTON.  
Holtzman MJ;  
WPI; 2002-566709/60.  
Use of RANTES chemokine or an expression system in treatment and diagnosis of paramyxovirus infection, especially in children -  
Claim 5; Page -; 19pp; English.  
The invention relates to the treatment of paramyxovirus infection that involves administration of an active ingredient such as RANTES chemokine (I) or an expression system (II). (I) and (II) are used in the treatment and diagnosis of paramyxoviral infection, especially in children. RANTES chemokine has a significant effect on respiratory infections caused by paramyxovirus. RANTES acts downstream of viral entry and signals through specific CCR1 and/or CCR5 chemokine receptors to interrupt the death pathway of macrophages which have been infected by virus. RANTES not only inhibits apoptosis of infected macrophage but also clears the macrophage of infection. The present sequence represents a human RANTES protein.  
Note: the present sequence is not provided in the specification. It has been obtained from the NCBI database under the accession no. NP\_002976.  
Sequence 91 AA;  
Query Match 98.7%; Score 472; DB 23; Length 91;  
Best Local Similarity 98.9%; Pred. No. 1.5e-45;  
Matches 90; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
1 MKVSAARLAVILLIATALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFYTSKGKCSNP 60  
1 MKVSAALAVILLIATALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFYTSKGKCSNP 60  
61 AVVFVTRKNQVCANPEKKWVREYINSLEMS 91  
61 AVVFVTRKNQVCANPEKKWVREYINSLEMS 91  
SULT 11  
221079  
AAO21079 standard; Protein; 91 AA.  
AAO21079;  
19-JUL-2002 (first entry)  
Wild type RANTES protein.  
RANTES; neuroprotective; antiallergic; antiinflammatory; anti-HIV; human; chemokine mutant; cationic site; multiple sclerosis; HIV infection; inflammatory disease; demyelinating disease; allergic; wild type.  
Homo sapiens.  
WO200238419-A2.  
11-APR-2002.  
03-OCT-2001; 2001WO-EP11428.  
04-OCT-2000; 2000EP-0121665.  
(ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.

XX Proudfoot A, Wells TNC, Kosco-Vilbois M;  
XX WPI; 2002-340073/37.  
XX A mutant of the human CC chemokine RANTES with two mutations in the cationic site of the 40's loop is used for treatment of multiple sclerosis and/or demyelinating diseases -  
XX Examples; Page 36; 46pp; English.  
XX The invention relates to a truncated and mutated human RANTES (a CC chemokine mutant), comprising the amino sequence of 91 amino acids as given in the specification. The CC chemokine mutant RANTES, with two mutations in the cationic site is useful for the preparation of a pharmaceutical composition used in treating multiple sclerosis or other demyelinating diseases. The mutant with single mutations at cationic sites is used for the treatment of HIV infection and/or other allergic or inflammatory diseases. This sequence represents the wild-type human RANTES protein of the invention.  
XX Sequence 91 AA;  
SQ Query Match 98.7%; Score 472; DB 23; Length 91;  
Best Local Similarity 98.9%; Pred. No. 1.5e-45;  
Matches 90; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MKVSAARLAVILLIATALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFYTSKGKCSNP 60  
Db 1 MKVSAALAVILLIATALCAPASASPYSSDTTPCCFAYIARPLPRAHIKEYFYTSKGKCSNP 60  
QY 61 AVVFVTRKNQVCANPEKKWVREYINSLEMS 91  
Db 61 AVVFVTRKNQVCANPEKKWVREYINSLEMS 91  
RESULT 12  
AAM52443  
ID AAM52443 standard; Protein; 91 AA.  
XX AAM52443;  
AC AAM52443;  
XX 03-JUL-2002 (first entry)  
XX HIV\_Nef1 fusion protein #10.  
DE Selenoprotein; HIV; Ebola virus; cancer; immune system disorder.  
XX Homo sapiens.  
OS US6303295-B1.  
PN US6303295-B1.  
XX 16-OCT-2001.  
PD 12-JUL-1996; 96US-0679493.  
PF 14-JUL-1995; 95US-001203P.  
XX 01-SEP-1995; 95US-003112P.  
PR (UYGE-) UNIV GEORGIA RES FOUND INC.  
XX Taylor EW, Nadimpalli RG, Ramanathan CS;  
PI WPI; 2002-024734/03.  
DR New selenoprotein for use in detecting certain viruses, e.g. human immunodeficiency virus (HIV) or Ebola, cancer and immune system disorders -  
XX Disclosure; Columns 73-76; 140pp; English.  
PS The present invention relates to selenoproteins encoded in the genome of a virus, where the coding sequence of the selenoprotein is genetically

C engineered for expression in a nucleic acid construct. The invention also  
C discloses a method for identifying selenoprotein coding sequences, for  
C detecting certain viruses (e.g. HIV or Ebola), cancer and immune system  
C disorders. The present sequence was used to illustrate the invention.

X Q Sequence 91 AA;  
Query Match 98.7%; Score 472; DB 23; Length 91;  
Best Local Similarity 98.9%; Pred. No. 1.5e-45;  
Matches 90; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 1 MKVSAARLAVILIATLALCAPASAPYSSDTPCCFAYIARPLPRAHIKEYFYTSKGKCSNP 60  
b 1 MKVSAALAVILIATLALCAPASAPYSSDTPCCFAYIARPLPRAHIKEYFYTSKGKCSNP 60

Y 61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91  
b 61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91

ESULT 13  
AO21086  
D AAO21086 standard; Protein; 91 AA.  
X AAO21086;  
X 19-JUL-2002 (first entry)  
E Protein of R44A-RANTES mutant.  
X RANTES; neuroprotective; antiallergic; antiinflammatory; anti-HIV; human;  
W chemokine mutant; cationic site; multiple sclerosis; HIV infection;  
W inflammatory disease; demyelinating disease; allergic; mutein.  
X Homo sapiens.  
S Synthetic.  
S WO200228419-A2.  
N 11-APR-2002.  
X 03-OCT-2001; 2001WO-EP11428.  
F 04-OCT-2000; 2000EP-0121665.  
X (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.  
X Proudfoot A, Wells TNC, Kosco-Vilbois M;  
X WPI; 2002-340073/37.

X A mutant of the human CC chemokine RANTES with two mutations in the  
T cationic site of the 40's loop is used for treatment of multiple  
T sclerosis and/or demyelinating diseases -  
X Examples; Page 39; 46pp; English.  
S The invention relates to a truncated and mutated human RANTES (a CC  
X chemokine mutant), comprising the amino sequence of 91 amino acids as  
C given in the specification. The CC chemokine mutant RANTES, with two  
C mutations in the cationic site is useful for the preparation of a  
C pharmaceutical composition used in treating multiple sclerosis or other  
C demyelinating diseases. The mutant with single mutations at cationic  
C sites is used for the treatment of HIV infection and/or other allergic or  
C inflammatory diseases. This sequence represents a mutant human RANTES  
C protein of the invention.

X Q Sequence 91 AA;  
Query Match 97.5%; Score 466; DB 23; Length 91;  
Best Local Similarity 97.8%; Pred. No. 6.9e-45;  
Matches 89; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MKVSAARLAVILIATLALCAPASAPYSSDTPCCFAYIARPLPRAHIKEYFYTSKGKCSNP 60  
Db 1 MKVSAALAVILIATLALCAPASAPYSSDTPCCFAYIARPLPRAHIKEYFYTSKGKCSNP 60  
QY 61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91  
Db 61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91

RESULT 14  
AAO21087  
ID AAO21087 standard; Protein; 91 AA.  
XX AAO21087;  
AC AAO21087;  
XX 19-JUL-2002 (first entry)  
DT Protein of K68A-RANTES mutant.  
DE  
XX RANTES; neuroprotective; antiallergic; antiinflammatory; anti-HIV; human;  
KW chemokine mutant; cationic site; multiple sclerosis; HIV infection;  
KW inflammatory disease; demyelinating disease; allergic; mutein.  
XX Homo sapiens.  
OS Synthetic.  
XX Key Location/Qualifiers  
FH Misc-difference 68 /note= "Wild-type Lys substituted by Ala"

FT WO200228419-A2.  
XX 11-APR-2002.  
XX 03-OCT-2001; 2001WO-EP11428.  
XX 04-OCT-2000; 2000EP-0121665.  
XX (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.  
PI Proudfoot A, Wells TNC, Kosco-Vilbois M;  
XX WPI; 2002-340073/37.  
DR A mutant of the human CC chemokine RANTES with two mutations in the  
XX cationic site of the 40's loop is used for treatment of multiple  
PT sclerosis and/or demyelinating diseases -  
XX Examples; Page 39; 46pp; English.  
XX The invention relates to a truncated and mutated human RANTES (a CC  
CC chemokine mutant), comprising the amino sequence of 91 amino acids as  
CC given in the specification. The CC chemokine mutant RANTES, with two  
CC mutations in the cationic site is useful for the preparation of a  
CC pharmaceutical composition used in treating multiple sclerosis or other  
CC demyelinating diseases. The mutant with single mutations at cationic  
CC sites is used for the treatment of HIV infection and/or other allergic or  
CC inflammatory diseases. This sequence represents a mutant human RANTES  
CC protein of the invention.

XX SQ Sequence 91 AA;  
Query Match 97.5%; Score 466; DB 23; Length 91;  
Best Local Similarity 97.8%; Pred. No. 6.9e-45;  
Matches 89; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MKVSAARLAVILIATLALCAPASAPYSSDTPCCFAYIARPLPRAHIKEYFYTSKGKCSNP 60  
Db 1 MKVSAALAVILIATLALCAPASAPYSSDTPCCFAYIARPLPRAHIKEYFYTSKGKCSNP 60  
QY 61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91  
Db 61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91



RESULT 15  
AO21088  
D AAO21088 standard; Protein; 91 AA.  
X  
C AAO21088;  
X  
T 19-JUL-2002 (first entry)  
X  
E Protein of R70A-RANTES mutant.  
X  
W RANTES; neuroprotective; antiallergic; antiinflammatory; anti-HIV; human;  
W chemokine mutant; cationic site; multiple sclerosis; HIV infection;  
W inflammatory disease; demyelinating disease; allergic; mutein.  
X  
S Homo sapiens.  
S Synthetic.  
X  
X  
H Key Location/Qualifiers  
T Misc-difference 70  
T /note= "Wild-type Arg substituted by Ala"  
X  
N WO200228419-A2.  
X  
D 11-APR-2002.  
X  
F 03-OCT-2001; 2001WO-EP11428.  
X  
R 04-OCT-2000; 2000EP-0121665.  
X  
A (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.  
X  
I Proudfoot A, Wells TNC, Kosco-Vilbois M;  
X WPI; 2002-340073/37.  
X  
T A mutant of the human CC chemokine RANTES with two mutations in the  
T cationic site of the 40's loop is used for treatment of multiple  
T sclerosis and/or demyelinating diseases -  
X  
S Examples; Page 40; 46pp; English.  
X  
C The invention relates to a truncated and mutated human RANTES (a CC  
C chemokine mutant), comprising the amino sequence of 91 amino acids as  
C given in the specification. The CC chemokine mutant RANTES, with two  
C mutations in the cationic site is useful for the preparation of a  
C pharmaceutical composition used in treating multiple sclerosis or other  
C demyelinating diseases. The mutant with single mutations at cationic  
C sites is used for the treatment of HIV infection and/or other allergic or  
C inflammatory diseases. This sequence represents a mutant human RANTES  
C protein of the invention.  
X  
X  
X Sequence 91 AA;  
Query Match 97.5%; Score 466; DB 23; Length 91;  
Best Local Similarity 97.8%; Pred. No. 6.9e-45;  
Matches 89; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
2Y 1 MKVSAARLAVILIATALCAPASAPSYSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNP 60  
2b 1 MKVSAARLAVILIATALCAPASAPSYSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNP 60  
2Y 61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91  
2b 61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91

Search completed: December 16, 2003, 15:37:49  
Job time : 37.3005 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

protein - protein search, using sw model

on: December 16, 2003, 15:39:40 ; Search time 24.3661 Seconds  
(without alignments)  
694.592 Million cell updates/sec

le: US-09-920-137A-8  
fect score: 478  
quence: 1 MKVSAARLAVILIATLALCAP.....VCANPEKKWVREYINSLEMS 91

ring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

arched: 684280 seqs, 185983659 residues

al number of hits satisfying chosen parameters: 684280

imum DB seq length: 0  
imum DB seq length: 2000000000

it-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

abase : Published Applications AA:\*  
1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*  
13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*  
17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

ult No.	Score	Query		DB ID	Description
		Match	Length		
1	478	100.0	91	8	US-08-927-939-21
2	478	100.0	91	9	US-09-144-838-9
3	478	100.0	91	9	US-09-834-795A-29
4	478	100.0	91	11	US-09-834-794A-29
5	478	100.0	91	11	US-09-920-137A-8
6	478	100.0	91	11	US-09-537-858-1
7	478	100.0	91	12	US-10-137-655-8
8	478	100.0	91	14	US-10-158-366-5
9	478	100.0	91	14	US-10-057-275-8
10	478	100.0	91	15	US-10-293-705-12
11	374	78.2	68	9	US-09-144-838-10
12	374	78.2	68	9	US-09-144-838-42
13	374	78.2	68	9	US-09-195-457-11
14	374	78.2	68	10	US-09-792-793A-29
15	374	78.2	68	12	US-10-375-209A-29

16	363.5	76.0	69	9	US-09-144-838-46	Sequence 46, Appl
17	363	75.9	66	11	US-09-537-858-2	Sequence 2, Appli
18	332	69.5	60	10	US-09-888-938-5	Sequence 5, Appli
19	325	68.0	67	9	US-09-144-838-38	Sequence 38, Appl
20	318	66.5	67	9	US-09-144-838-41	Sequence 41, Appl
21	317	66.3	68	9	US-09-144-838-40	Sequence 40, Appl
22	316	66.1	68	9	US-09-144-838-34	Sequence 34, Appl
23	307.5	64.3	68	9	US-09-144-838-45	Sequence 45, Appl
24	306.5	64.1	69	9	US-09-144-838-44	Sequence 44, Appl
25	269	56.3	66	9	US-09-144-838-37	Sequence 37, Appl
26	268	56.1	67	9	US-09-144-838-36	Sequence 36, Appl
27	261	54.6	67	9	US-09-144-838-39	Sequence 39, Appl
28	260	54.4	67	9	US-09-144-838-33	Sequence 33, Appl
29	259	54.2	68	9	US-09-144-838-32	Sequence 32, Appl
30	252.5	52.8	93	8	US-08-927-939-49	Sequence 49, Appl
31	252.5	52.8	93	9	US-09-151-450-2	Sequence 2, Appli
32	252.5	52.8	93	9	US-09-834-795A-32	Sequence 32, Appl
33	252.5	52.8	93	11	US-09-834-794A-32	Sequence 32, Appli
34	252.5	52.8	93	12	US-10-260-270-3	Sequence 3, Appli
35	252.5	52.8	93	12	US-10-223-081-330	Sequence 330, App
36	252.5	52.8	93	12	US-10-223-082-330	Sequence 330, App
37	252.5	52.8	93	12	US-10-247-671-179	Sequence 179, App
38	252.5	52.8	93	14	US-10-141-965-6	Sequence 6, Appli
39	252.5	52.8	93	15	US-10-223-085-330	Sequence 330, App
40	252.5	52.8	93	15	US-10-223-084-330	Sequence 330, App
41	252.5	52.8	93	15	US-10-223-088-330	Sequence 330, App
42	252.5	52.8	93	15	US-10-223-090-330	Sequence 330, App
43	252.5	52.8	93	15	US-10-223-087-330	Sequence 330, App
44	252.5	52.8	93	15	US-10-223-083-330	Sequence 330, App
45	252.5	52.8	93	15	US-10-223-089-330	Sequence 330, App

ALIGNMENTS

RESULT 1  
US-08-927-939-21  
; Sequence 21, Application US/08927939  
; Publication No. US20010006640A1  
; GENERAL INFORMATION:  
; APPLICANT: Grainger, David J.  
; APPLICANT: Tatalick, Lauen Marie  
; TITLE OF INVENTION: Compounds and methods to inhibit or  
; TITLE OF INVENTION: augment an inflammatory response.  
; FILE REFERENCE: 295.022US1  
; CURRENT APPLICATION NUMBER: US/08/927,939  
; CURRENT FILING DATE: 1997-09-11  
; NUMBER OF SEQ ID NOS: 83  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 21  
; LENGTH: 91  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-08-927-939-21

Query Match 100.0%; Score 478; DB 8; Length 91;  
Best Local Similarity 100.0%; Pred. NO. 6.4e-47;  
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MKVSAARLAVILIATLALCAPASAPSYSDTTPCCFAYIARPLPRAHIKEYFTSGKCSNP	60
Db	1	MKVSAARLAVILIATLALCAPASAPSYSDTTPCCFAYIARPLPRAHIKEYFTSGKCSNP	60
Qy	61	AWFVTRKNRQVCANPEKKWVREYINSLEMS	91
Db	61	AWFVTRKNRQVCANPEKKWVREYINSLEMS	91

RESULT 2  
US-09-144-838-9  
; Sequence 9, Application US/09144838A  
; Patent No. US20020051996A1  
; GENERAL INFORMATION:

APPLICANT: Siani, Michael A.  
APPLICANT: Wilken, Jill  
APPLICANT: Simon, Reyna  
APPLICANT: Kent, Stephen B.H.  
TITLE OF INVENTION: Modular Protein Libraries and Methods of Preparation  
FILE REFERENCE: GRFN-020/01US  
CURRENT APPLICATION NUMBER: US/09/144,838A  
CURRENT FILING DATE: 1998-08-31  
EARLIER APPLICATION NUMBER: US 60/057,620  
EARLIER FILING DATE: 1997-09-04  
NUMBER OF SEQ ID NOS: 54  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 9  
LENGTH: 91  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
-09-144-838-9

Query Match 100.0%; Score 478; DB 9; Length 91;  
Best Local Similarity 100.0%; Pred. No. 6.4e-47;  
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
1 MKVSAARLAVILIATLALCAPASASPYSSDTPCCFAYIARPLPRAHIKEYFTSGKCSNP 60  
|||||  
1 MKVSAARLAVILIATLALCAPASASPYSSDTPCCFAYIARPLPRAHIKEYFTSGKCSNP 60  
|||||  
61 AVFVTRKNRQVCANPEKKWVREYINSLEMS 91  
|||||  
61 AVFVTRKNRQVCANPEKKWVREYINSLEMS 91  
|||||

SULT 3  
-09-834-795A-29  
Sequence 29, Application US/09834795A  
Patent No. US20020076710A1  
GENERAL INFORMATION:

APPLICANT: Lawrence, Papsidero  
APPLICANT: Lyn, Dyster  
APPLICANT: Jana, Frustaci  
TITLE OF INVENTION: Detection and Treatment of Breast Cancer  
FILE REFERENCE: 3380/11127-US3  
CURRENT APPLICATION NUMBER: US/09/834,795A  
CURRENT FILING DATE: 2001-04-12  
PRIOR APPLICATION NUMBER: 09/146,580  
PRIOR FILING DATE: 1998-09-03  
PRIOR APPLICATION NUMBER: 60/071,899  
PRIOR FILING DATE: 1998-01-20  
PRIOR APPLICATION NUMBER: 60/092,155  
PRIOR FILING DATE: 1998-07-09  
NUMBER OF SEQ ID NOS: 35  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 29  
LENGTH: 91  
TYPE: PRT  
ORGANISM: Homo sapiens  
-09-834-795A-29

Query Match 100.0%; Score 478; DB 9; Length 91;  
Best Local Similarity 100.0%; Pred. No. 6.4e-47;  
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
1 MKVSAARLAVILIATLALCAPASASPYSSDTPCCFAYIARPLPRAHIKEYFTSGKCSNP 60  
|||||  
1 MKVSAARLAVILIATLALCAPASASPYSSDTPCCFAYIARPLPRAHIKEYFTSGKCSNP 60  
|||||  
61 AVFVTRKNRQVCANPEKKWVREYINSLEMS 91  
|||||  
61 AVFVTRKNRQVCANPEKKWVREYINSLEMS 91  
|||||

SULT 4

US-09-834-794A-29  
Sequence 29, Application US/09834794A  
Publication No. US20030026777A1  
GENERAL INFORMATION:  
APPLICANT: Lawrence, Papsidero  
APPLICANT: Lyn, Dyster  
APPLICANT: Jana, Frustaci  
TITLE OF INVENTION: Detection and Treatment of Breast Cancer  
FILE REFERENCE: 3380/11127-US4  
CURRENT APPLICATION NUMBER: US/09/834,794A  
CURRENT FILING DATE: 2001-04-13  
PRIOR APPLICATION NUMBER: 09/146,580  
PRIOR FILING DATE: 1998-09-03  
PRIOR APPLICATION NUMBER: 60/071,899  
PRIOR FILING DATE: 1998-01-20  
PRIOR APPLICATION NUMBER: 60/092,155  
PRIOR FILING DATE: 1998-07-09  
NUMBER OF SEQ ID NOS: 35  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 29  
LENGTH: 91  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-834-794A-29

Query Match 100.0%; Score 478; DB 11; Length 91;  
Best Local Similarity 100.0%; Pred. No. 6.4e-47;  
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MKVSAARLAVILIATLALCAPASASPYSSDTPCCFAYIARPLPRAHIKEYFTSGKCSNP 60  
|||||  
Db 1 MKVSAARLAVILIATLALCAPASASPYSSDTPCCFAYIARPLPRAHIKEYFTSGKCSNP 60  
|||||  
QY 61 AVFVTRKNRQVCANPEKKWVREYINSLEMS 91  
|||||  
Db 61 AVFVTRKNRQVCANPEKKWVREYINSLEMS 91  
|||||

RESULT 5

US-09-920-137A-8  
Sequence 8, Application US/09920137A  
Publication No. US20030049725A1  
GENERAL INFORMATION:  
APPLICANT: Coleman, Roger  
APPLICANT: Bandman, Olga  
APPLICANT: Wilde, Craig G.  
TITLE OF INVENTION: NEW CHEMOKINES EXPRESSED IN PANCREAS  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/920,137A  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Luther, Barbara J.  
REGISTRATION NUMBER: 33,954  
REFERENCE/DOCKET NUMBER: PF-0027 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-852-0195  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 91 amino acids

TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: RANTES  
-09-920-137A-8

Query Match 100.0%; Score 478; DB 11; Length 91;  
Best Local Similarity 100.0%; Pred. No. 6.4e-47;  
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKVSAARLAVILIATLALCAPASAPSYSSDTPCCFAYIARPLPRAHIKEYFYTSKGKCSNP 60  
|||||  
1 MKVSAARLAVILIATLALCAPASAPSYSSDTPCCFAYIARPLPRAHIKEYFYTSKGKCSNP 60

61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91  
|||||  
61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91

SULT 6  
-09-537-858-1  
Sequence 1, Application US/09537858  
Publication No. US20030119148A1  
GENERAL INFORMATION:  
APPLICANT: PROOST, PAUL  
APPLICANT: STRUYF, SOFIE  
APPLICANT: VAN DAMME, JO  
TITLE OF INVENTION: AMINO-TERMINALLY TRUNCATED RANTES AS CHEMOKINE  
FILE OF INVENTION: ANTAGONISTS  
CURRENT APPLICATION NUMBER: US/09/537,858  
CURRENT FILING DATE: 2001-02-26  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: PatentIn ver. 2.1  
SEQ ID NO 1  
LENGTH: 91  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: peptide  
-09-537-858-1

Query Match 100.0%; Score 478; DB 11; Length 91;  
Best Local Similarity 100.0%; Pred. No. 6.4e-47;  
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKVSAARLAVILIATLALCAPASAPSYSSDTPCCFAYIARPLPRAHIKEYFYTSKGKCSNP 60  
|||||  
1 MKVSAARLAVILIATLALCAPASAPSYSSDTPCCFAYIARPLPRAHIKEYFYTSKGKCSNP 60

61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91  
|||||  
61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91

SULT 7  
-10-137-655-8  
Sequence 8, Application US/10137655  
Publication No. US20030138917A1  
GENERAL INFORMATION:  
APPLICANT: Coleman, Roger  
APPLICANT: Bandman, Olga  
APPLICANT: Wilde, Craig G.  
TITLE OF INVENTION: NEW CHEMOKINES EXPRESSED IN PANCREAS  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto

STATE: CA  
COUNTRY: U.S.  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/137,655  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Luther, Barbara J.  
REGISTRATION NUMBER: 33,954  
REFERENCE/DOCKET NUMBER: PF-0027 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-852-0195  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 91 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: RANTES  
US-10-137-655-8

Query Match 100.0%; Score 478; DB 12; Length 91;  
Best Local Similarity 100.0%; Pred. No. 6.4e-47;  
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKVSAARLAVILIATLALCAPASAPSYSSDTPCCFAYIARPLPRAHIKEYFYTSKGKCSNP 60  
|||||  
Db 1 MKVSAARLAVILIATLALCAPASAPSYSSDTPCCFAYIARPLPRAHIKEYFYTSKGKCSNP 60

QY 61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91  
|||||  
Db 61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91

RESULT 8  
US-10-158-366-5  
Sequence 5, Application US/10158366  
Publication No. US20020142398A1  
GENERAL INFORMATION:  
APPLICANT: Coleman, Roger  
Wilde, Craig C.  
Seilhamer, Jeffrey J.  
TITLE OF INVENTION: CHEMOKINE EXPRESSED IN FETAL SPLEEN,  
ITS PRODUCTION AND USES  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/158,366  
FILING DATE: 29-May-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,123B  
FILING DATE: 06-JUN-1995



APPLICATION NUMBER: US 08/375,346  
FILING DATE: 19-JAN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0026-1 DIV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-555-0555  
TELEFAX: 415-845-4166  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 91 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
-10-158-366-5

Query Match 100.0%; Score 478; DB 14; Length 91;  
Best Local Similarity 100.0%; Pred. No. 6.4e-47;  
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 MKVSAARLAVILIATLALCAPASAPYSSDTPCCFAYIARPLPRAHIKEYFTSGKCSNP 60  
1 MKVSAARLAVILIATLALCAPASAPYSSDTPCCFAYIARPLPRAHIKEYFTSGKCSNP 60  
61 AVVFVTRKNQVCANPEKKWVREYINSLEMS 91  
61 AVVFVTRKNQVCANPEKKWVREYINSLEMS 91

SULT 9  
-10-057-275-8  
Sequence 8, Application US/10057275  
Publication No. US20020155545A1  
GENERAL INFORMATION:  
APPLICANT: Coleman, Roger  
Bandman, Olga  
Wilde, Craig G.  
TITLE OF INVENTION: NEW CHEMOKINES EXPRESSED IN PANCREAS  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.  
ZIP: 94304

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/057,275  
FILING DATE: 25-Jan-2002  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/390,740A  
FILING DATE: February 17, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Luther, Barbara J.  
REGISTRATION NUMBER: 33,954  
REFERENCE/DOCKET NUMBER: PF-0027 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-852-0195  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 91 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

; MOLECULE TYPE: peptide  
; IMMEDIATE SOURCE:  
; LIBRARY: GenBank  
; CLONE: RANTES  
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:  
US-10-057-275-8  
Query Match 100.0%; Score 478; DB 14; Length 91;  
Best Local Similarity 100.0%; Pred. No. 6.4e-47;  
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKVSAARLAVILIATLALCAPASAPYSSDTPCCFAYIARPLPRAHIKEYFTSGKCSNP 60  
Db 1 MKVSAARLAVILIATLALCAPASAPYSSDTPCCFAYIARPLPRAHIKEYFTSGKCSNP 60  
QY 61 AVVFVTRKNQVCANPEKKWVREYINSLEMS 91  
Db 61 AVVFVTRKNQVCANPEKKWVREYINSLEMS 91

RESULT 10  
US-10-293-705-12  
; Sequence 12, Application US/10293705  
; Publication No. US20030083468A1  
; GENERAL INFORMATION:  
; APPLICANT: Wilde, Craig G.  
; APPLICANT: Hawkins, Phillip R.  
; APPLICANT: Bandman, Olga  
; APPLICANT: Seilhamer, Jeffrey J.  
; TITLE OF INVENTION: DNA ENCODING LIVER EXPRESSED CHEMOKINE  
; FILE REFERENCE: PF-0024-3 CON  
; CURRENT APPLICATION NUMBER: US/10/293,705  
; CURRENT FILING DATE: 2002-11-12  
; PRIOR APPLICATION NUMBER: 09/208,803  
; PRIOR FILING DATE: 1998-12-09  
; PRIOR APPLICATION NUMBER: 08/798,143  
; PRIOR FILING DATE: 1997-02-10  
; PRIOR APPLICATION NUMBER: 08/347,492  
; PRIOR FILING DATE: 1994-11-29  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PERL Program  
; SEQ ID NO 12  
; LENGTH: 91  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: GenBank ID No. US20030083468A1 g134510  
US-10-293-705-12

Query Match 100.0%; Score 478; DB 15; Length 91;  
Best Local Similarity 100.0%; Pred. No. 6.4e-47;  
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKVSAARLAVILIATLALCAPASAPYSSDTPCCFAYIARPLPRAHIKEYFTSGKCSNP 60  
Db 1 MKVSAARLAVILIATLALCAPASAPYSSDTPCCFAYIARPLPRAHIKEYFTSGKCSNP 60  
QY 61 AVVFVTRKNQVCANPEKKWVREYINSLEMS 91  
Db 61 AVVFVTRKNQVCANPEKKWVREYINSLEMS 91

RESULT 11  
US-09-144-838-10  
; Sequence 10, Application US/09144838A  
; Patent No. US20020051996A1  
; GENERAL INFORMATION:  
; APPLICANT: Siani, Michael A.  
; APPLICANT: Wilken, Jill  
; APPLICANT: Simon, Reyna  
; APPLICANT: Kent, Stephen B.H.  
; TITLE OF INVENTION: Modular Protein Libraries and Methods of Preparation

FILE REFERENCE: GRFN-020/01US  
CURRENT APPLICATION NUMBER: US/09/144,838A  
CURRENT FILING DATE: 1998-08-31  
EARLIER APPLICATION NUMBER: US 60/057,620  
EARLIER FILING DATE: 1997-09-04  
NUMBER OF SEQ ID NOS: 54  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 10  
LENGTH: 68  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
-09-144-838-10

Query Match 78.2%; Score 374; DB 9; Length 68;  
Best Local Similarity 100.0%; Pred. No. 3.2e-35;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

24 SPYSSDTPCCFAYIARPLPRAHIKEYFTSGKCSNPVAVFVTRKNRQVCANPEKKWVRE 83  
|||||  
1 SPYSSDTPCCFAYIARPLPRAHIKEYFTSGKCSNPVAVFVTRKNRQVCANPEKKWVRE 60  
|||||

84 YINSLEMS 91  
|||||  
61 YINSLEMS 68

## SULT 12

-09-144-838-42  
Sequence 42, Application US/09144838A  
Patent No. US20020051996A1

## GENERAL INFORMATION:

APPLICANT: Siani, Michael A.  
APPLICANT: Wilken, Jill  
APPLICANT: Simon, Reyna  
APPLICANT: Kent, Stephen B.H.  
TITLE OF INVENTION: Modular Protein Libraries and Methods of Preparation  
FILE REFERENCE: GRFN-020/01US  
CURRENT APPLICATION NUMBER: US/09/144,838A  
CURRENT FILING DATE: 1998-08-31  
EARLIER APPLICATION NUMBER: US 60/057,620  
EARLIER FILING DATE: 1997-09-04  
NUMBER OF SEQ ID NOS: 54  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 42  
LENGTH: 68  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
-09-144-838-42

Query Match 78.2%; Score 374; DB 9; Length 68;  
Best Local Similarity 100.0%; Pred. No. 3.2e-35;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

24 SPYSSDTPCCFAYIARPLPRAHIKEYFTSGKCSNPVAVFVTRKNRQVCANPEKKWVRE 83  
|||||  
1 SPYSSDTPCCFAYIARPLPRAHIKEYFTSGKCSNPVAVFVTRKNRQVCANPEKKWVRE 60  
|||||

84 YINSLEMS 91  
|||||  
61 YINSLEMS 68

## SULT 13

-09-195-457-11  
Sequence 11, Application US/09195457  
Patent No. US20020081623A1

## GENERAL INFORMATION:

APPLICANT: WILLIAMS, TIMOTHY J.  
APPLICANT: JOSE, PETER J.

APPLICANT: GRIFFITHS-JOHNSON, DAVID A.  
APPLICANT: HSUAN, JOHN J.  
TITLE OF INVENTION: CHEMOTACTIC CYTOKINE  
FILE REFERENCE: 550-33  
CURRENT APPLICATION NUMBER: US/09/195,457  
CURRENT FILING DATE: 1998-11-18  
PRIOR APPLICATION NUMBER: 08/470,323  
PRIOR FILING DATE: 1995-06-06  
PRIOR APPLICATION NUMBER: PCT/GB94/02006  
PRIOR FILING DATE: 1994-09-14  
PRIOR APPLICATION NUMBER: GB 9318984.3  
PRIOR FILING DATE: 1993-09-14  
PRIOR APPLICATION NUMBER: GB 94086902.2  
PRIOR FILING DATE: 1994-04-29  
NUMBER OF SEQ ID NOS: 11  
SEQ ID NO 11  
LENGTH: 68  
TYPE: PRT  
ORGANISM: human  
US-09-195-457-11

Query Match 78.2%; Score 374; DB 9; Length 68;  
Best Local Similarity 100.0%; Pred. No. 3.2e-35;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 SPYSSDTPCCFAYIARPLPRAHIKEYFTSGKCSNPVAVFVTRKNRQVCANPEKKWVRE 83  
|||||  
Db 1 SPYSSDTPCCFAYIARPLPRAHIKEYFTSGKCSNPVAVFVTRKNRQVCANPEKKWVRE 60  
|||||

QY 84 YINSLEMS 91  
|||||  
Db 61 YINSLEMS 68

## RESULT 14

US-09-792-793A-29  
Sequence 29, Application US/09792793A  
Patent No. US20020168370A1

## GENERAL INFORMATION:

APPLICANT: McDonald, John R.  
APPLICANT: Coggins, Philip  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE A  
TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS  
FILE REFERENCE: 25020-601D  
CURRENT APPLICATION NUMBER: US/09/792,793A  
CURRENT FILING DATE: 2001-02-22  
NUMBER OF SEQ ID NOS: 93  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 29  
LENGTH: 68  
TYPE: PRT  
ORGANISM: homo sapien  
FEATURE:  
OTHER INFORMATION: Human Chemokine Polypeptide: RANTES  
US-09-792-793A-29

Query Match 78.2%; Score 374; DB 10; Length 68;  
Best Local Similarity 100.0%; Pred. No. 3.2e-35;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 SPYSSDTPCCFAYIARPLPRAHIKEYFTSGKCSNPVAVFVTRKNRQVCANPEKKWVRE 83  
|||||  
Db 1 SPYSSDTPCCFAYIARPLPRAHIKEYFTSGKCSNPVAVFVTRKNRQVCANPEKKWVRE 60  
|||||

QY 84 YINSLEMS 91  
|||||  
Db 61 YINSLEMS 68

## RESULT 15

US-10-375-209A-29

Sequence 29, Application US/10375209A  
Publication No. US20030215421A1

GENERAL INFORMATION:  
APPLICANT: McDonald, John R.  
APPLICANT: Coggins, Philip  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND  
TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS  
FILE REFERENCE: 25020-601E  
CURRENT APPLICATION NUMBER: US/10/375,209A  
CURRENT FILING DATE: 2003-02-24  
NUMBER OF SEQ ID NOS: 93  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 29  
LENGTH: 68  
TYPE: PRT  
ORGANISM: homo sapien  
FEATURE:  
OTHER INFORMATION: Human Chemokine Polypeptide: RANTES  
-10-375-209A-29  
Query Match 78.2%; Score 374; DB 12; Length 68;  
Best Local Similarity 100.0%; Pred. No. 3.2e-35;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
24 SPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNPVAVVTRKNRQVCANPEKKWVRE 83  
|||||  
1 SPYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNPVAVVTRKNRQVCANPEKKWVRE 60  
|||||  
84 YINSLEMS 91  
|||||  
61 YINSLEMS 68  
arch completed: December 16, 2003, 15:48:25  
b time : 25.3661 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.  
protein - protein search, using sw model  
on: December 16, 2003, 15:37:55 ; Search time 165.59 Seconds  
(without alignments)  
500.045 Million cell updates/sec  
le: US-09-920-137A-8  
fect score: 478  
quence: 1 MKVSAARLAVILIATLALCAP.....VCANPEKKWREYINSLEMS 91  
oring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
arched: 5728757 seqs, 909918778 residues  
al number of hits satisfying chosen parameters: 5728757  
imum DB seq length: 0  
imum DB seq length: 2000000000  
st-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

abase : Pending Patents AA Main: \*  
1: /cgn2\_6/ptodata/1/paa/ptorus COMB.pep: \*  
2: /cgn2\_6/ptodata/1/paa/US06 COMB.pep: \*  
3: /cgn2\_6/ptodata/1/paa/US07 COMB.pep: \*  
4: /cgn2\_6/ptodata/1/paa/US08 COMB.pep: \*  
5: /cgn2\_6/ptodata/1/paa/US081 COMB.pep: \*  
6: /cgn2\_6/ptodata/1/paa/US082 COMB.pep: \*  
7: /cgn2\_6/ptodata/1/paa/US083 COMB.pep: \*  
8: /cgn2\_6/ptodata/1/paa/US084 COMB.pep: \*  
9: /cgn2\_6/ptodata/1/paa/US085 COMB.pep: \*  
10: /cgn2\_6/ptodata/1/paa/US086 COMB.pep: \*  
11: /cgn2\_6/ptodata/1/paa/US087 COMB.pep: \*  
12: /cgn2\_6/ptodata/1/paa/US088 COMB.pep: \*  
13: /cgn2\_6/ptodata/1/paa/US089 COMB.pep: \*  
14: /cgn2\_6/ptodata/1/paa/US090 COMB.pep: \*  
15: /cgn2\_6/ptodata/1/paa/US091 COMB.pep: \*  
16: /cgn2\_6/ptodata/1/paa/US092 COMB.pep: \*  
17: /cgn2\_6/ptodata/1/paa/US093 COMB.pep: \*  
18: /cgn2\_6/ptodata/1/paa/US094 COMB.pep: \*  
19: /cgn2\_6/ptodata/1/paa/US095 COMB.pep: \*  
20: /cgn2\_6/ptodata/1/paa/US096 COMB.pep: \*  
21: /cgn2\_6/ptodata/1/paa/US097A COMB.pep: \*  
22: /cgn2\_6/ptodata/1/paa/US097B COMB.pep: \*  
23: /cgn2\_6/ptodata/1/paa/US098 COMB.pep: \*  
24: /cgn2\_6/ptodata/1/paa/US099A COMB.pep: \*  
25: /cgn2\_6/ptodata/1/paa/US099B COMB.pep: \*  
26: /cgn2\_6/ptodata/1/paa/US100 COMB.pep: \*  
27: /cgn2\_6/ptodata/1/paa/US101 COMB.pep: \*  
28: /cgn2\_6/ptodata/1/paa/US102 COMB.pep: \*  
29: /cgn2\_6/ptodata/1/paa/US103 COMB.pep: \*  
30: /cgn2\_6/ptodata/1/paa/US104 COMB.pep: \*  
31: /cgn2\_6/ptodata/1/paa/US106 COMB.pep: \*  
32: /cgn2\_6/ptodata/1/paa/US60 COMB.pep: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	478	100.0	91	1	PCT-US94-08207A-36 Sequence 36, Appl

2	478	100.0	91	1	PCT-US94-08207-36
3	478	100.0	91	5	US-08-136-117-36
4	478	100.0	91	7	US-08-390-740B-8
5	478	100.0	91	8	US-08-467-123-5
6	478	100.0	91	13	US-08-927-939-21
7	478	100.0	91	13	US-08-927-939A-21
8	478	100.0	91	14	US-09-023-092-4
9	478	100.0	91	15	US-09-113-705-8
10	478	100.0	91	15	US-09-113-705-5
11	478	100.0	91	15	US-09-144-838-9
12	478	100.0	91	15	US-09-150-813-21
13	478	100.0	91	16	US-09-208-803-12
14	478	100.0	91	17	US-09-360-290-5
15	478	100.0	91	17	US-09-387-620-5
16	478	100.0	91	19	US-09-537-858-1
17	478	100.0	91	19	US-09-537-858B-1
18	478	100.0	91	19	US-09-537-858C-1
19	478	100.0	91	22	US-09-791-537-22750
20	478	100.0	91	23	US-09-834-794A-29
21	478	100.0	91	23	US-09-834-795A-29
22	478	100.0	91	24	US-09-920-137A-8
23	478	100.0	91	26	US-10-057-275-8
24	478	100.0	91	27	US-10-137-655-8
25	478	100.0	91	27	US-10-158-366-5
26	478	100.0	91	28	US-10-293-705-12
27	478	100.0	444	1	PCT-US01-08656-8708
28	478	100.0	444	28	US-10-273-573-8708
29	472	98.7	91	8	US-08-479-620-21
30	472	98.7	91	9	US-08-558-658-21
31	472	98.7	91	10	US-08-622-851A-16
32	472	98.7	91	14	US-09-067-447-21
33	472	98.7	91	14	US-09-067-447-21
34	472	98.7	91	14	US-09-067-447B-21
35	472	98.7	91	19	US-09-509-165A-21
36	472	98.7	91	22	US-09-791-537-115540
37	472	98.7	91	23	US-09-872-611-16
38	472	98.7	91	28	US-10-276-781-1528
39	472	98.7	91	28	US-10-295-027-1232
40	472	98.7	91	29	US-10-325-899-9334
41	472	98.7	91	31	US-10-601-072-289
42	472	98.7	91	32	US-60-453-050-13789
43	472	98.7	91	32	US-60-453-135-13789
44	472	98.7	91	32	US-60-455-444-7331
45	472	98.7	91	32	US-60-465-241-7331

ALIGNMENTS

RESULT 1

PCT-US94-08207A-36

; Sequence 36, Application PC/TUS9408207A

; GENERAL INFORMATION:

; APPLICANT: The Upjohn Company

; APPLICANT: FOR U.S. PURPOSES ONLY: Hoogewerf, Arlene J. and Ledbetter, Steven R.

; TITLE OF INVENTION: USE OF HEPARANASE TO IDENTIFY AND

; TITLE OF INVENTION: ISOLATE ANTI-HEPARANASE COMPOUNDS

; NUMBER OF SEQUENCES: 43

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: The Upjohn Company, Intellectual Property Law

; STREET: 301 Henrietta

; CITY: Kalamazoo

; STATE: MI

; COUNTRY: USA

; ZIP: 49001

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US94/08207A

; FILING DATE:



Tue Dec 16 15:54:10 2003

CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Jameson, William G.  
REGISTRATION NUMBER: 27,199  
REFERENCE/DOCKET NUMBER: 4731.1 CP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 616/385-7561  
TELEFAX: 616/385-6897  
TELEX: 224401  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 91 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
T-US94-08207A-36

Query Match 100.0%; Score 478; DB 1; Length 91;  
Best Local Similarity 100.0%; Pred. No. 2.9e-46;  
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKVSAARLAVILIATALCAPASAPSYSSDTPCCFAYIARPLPRAHIKEYFYTSGKCSNP 60  
|||||  
1 MKVSAARLAVILIATALCAPASAPSYSSDTPCCFAYIARPLPRAHIKEYFYTSGKCSNP 60  
|||||

61 AVFVTRKNRQVCANPEKKWVREYINSLEMS 91  
|||||  
61 AVFVTRKNRQVCANPEKKWVREYINSLEMS 91  
|||||

RESULT 2  
T-US94-08207-36  
Sequence 36, Application PC/TUS9408207  
GENERAL INFORMATION:  
APPLICANT: Hoogewerf, Arlene J.  
APPLICANT: Ledbetter, Steven R.  
TITLE OF INVENTION: USE OF HEPARANASE TO IDENTIFY AND  
TITLE OF INVENTION: ISOLATE ANTI-HEPARANASE COMPOUNDS  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: The Upjohn Company, Intellectual Property Law  
STREET: 301 Henrietta  
CITY: Kalamazoo  
STATE: MI  
COUNTRY: USA  
ZIP: 49001  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/08207  
FILING DATE:

CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Jameson, William G.  
REGISTRATION NUMBER: 27,199  
REFERENCE/DOCKET NUMBER: 4731.1 CP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 616/385-7561  
TELEFAX: 616/385-6897  
TELEX: 224401  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 91 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
T-US94-08207-36

T-US94-08207-36

Query Match 100.0%; Score 478; DB 1; Length 91;  
Best Local Similarity 100.0%; Pred. No. 2.9e-46;  
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKVSAARLAVILIATALCAPASAPSYSSDTPCCFAYIARPLPRAHIKEYFYTSGKCSNP 60  
|||||  
1 MKVSAARLAVILIATALCAPASAPSYSSDTPCCFAYIARPLPRAHIKEYFYTSGKCSNP 60  
|||||

61 AVFVTRKNRQVCANPEKKWVREYINSLEMS 91  
|||||  
61 AVFVTRKNRQVCANPEKKWVREYINSLEMS 91  
|||||

RESULT 3  
US-08-136-117-36  
Sequence 36, Application US/08136117  
GENERAL INFORMATION:  
APPLICANT: Hoogewerf, Arlene J.  
APPLICANT: Ledbetter, Steven R.  
TITLE OF INVENTION: USE OF HEPARANASE TO IDENTIFY AND  
TITLE OF INVENTION: ISOLATE ANTI-HEPARANASE COMPOUNDS  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: The Upjohn Company, Intellectual Property Law  
STREET: 301 Henrietta  
CITY: Kalamazoo  
STATE: MI  
COUNTRY: USA  
ZIP: 49001  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/136,117  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Jameson, William G.  
REGISTRATION NUMBER: 27,199  
REFERENCE/DOCKET NUMBER: 4731.1 CP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 616/385-7561  
TELEFAX: 616/385-6897  
TELEX: 224401  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 91 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-136-117-36

Query Match 100.0%; Score 478; DB 5; Length 91;  
Best Local Similarity 100.0%; Pred. No. 2.9e-46;  
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKVSAARLAVILIATALCAPASAPSYSSDTPCCFAYIARPLPRAHIKEYFYTSGKCSNP 60  
|||||  
1 MKVSAARLAVILIATALCAPASAPSYSSDTPCCFAYIARPLPRAHIKEYFYTSGKCSNP 60  
|||||

61 AVFVTRKNRQVCANPEKKWVREYINSLEMS 91  
|||||  
61 AVFVTRKNRQVCANPEKKWVREYINSLEMS 91  
|||||

RESULT 4  
US-08-390-740B-8  
Sequence 8, Application US/08390740B  
GENERAL INFORMATION:  
APPLICANT: Coleman, Roger

APPLICANT: Bandman, Olga  
APPLICANT: Wilde, Craig G.  
TITLE OF INVENTION: NEW CHEMOKINES EXPRESSED IN PANCREAS  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.  
ZIP: 94304

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/390,740B  
FILING DATE:

ATTORNEY/AGENT INFORMATION:  
NAME: Luther, Barbara J.  
REGISTRATION NUMBER: 33,954  
REFERENCE/DOCKET NUMBER: PF-0027 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-852-0195

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:  
LENGTH: 91 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: RANTES

-08-390-740B-8

Query Match 100.0%; Score 478; DB 7; Length 91;  
Best Local Similarity 100.0%; Pred. No. 2.9e-46;  
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKVSAARLAVILIATLALCAPASAPYSSDTPCCFAYIARPLPRAHIKEYFTSGKCSNP 60  
|||||  
1 MKVSAARLAVILIATLALCAPASAPYSSDTPCCFAYIARPLPRAHIKEYFTSGKCSNP 60

61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91  
|||||

61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91  
|||||

SULT 5

-08-467-123-5  
Sequence 5, Application US/08467123

GENERAL INFORMATION:  
APPLICANT: Coleman, Roger  
APPLICANT: Wilde, Craig G.  
APPLICANT: Seilhamer, Jeffrey J.  
TITLE OF INVENTION: A NEW CHEMOKINE EXPRESSED IN FETAL SPLEEN,  
ITS PRODUCTION AND USES  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3330 HILLVIEW AVENUE  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,123  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/375,346  
FILING DATE: 19-JAN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: LUTHER, BARBARA J.  
REGISTRATION NUMBER: 33,954  
REFERENCE/DOCKET NUMBER: PF-0026 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 855-0555  
TELEFAX: (415) 855-0572  
TELEX:

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:  
LENGTH: 91 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:

US-08-467-123-5

Query Match 100.0%; Score 478; DB 8; Length 91;  
Best Local Similarity 100.0%; Pred. No. 2.9e-46;  
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKVSAARLAVILIATLALCAPASAPYSSDTPCCFAYIARPLPRAHIKEYFTSGKCSNP 60  
|||||

Db 1 MKVSAARLAVILIATLALCAPASAPYSSDTPCCFAYIARPLPRAHIKEYFTSGKCSNP 60  
|||||

QY 61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91  
|||||

Db 61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91  
|||||

RESULT 6

US-08-927-939-21

Sequence 21, Application US/08927939

GENERAL INFORMATION:

APPLICANT: Grainger, David J.  
APPLICANT: Tatalick, Lauen Marie  
TITLE OF INVENTION: Compounds and methods to inhibit or  
augment an inflammatory response.  
FILE REFERENCE: 295.022US1  
CURRENT APPLICATION NUMBER: US/08/927,939  
CURRENT FILING DATE: 1997-09-11  
NUMBER OF SEQ ID NOS: 83  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 21

LENGTH: 91

TYPE: PRT

ORGANISM: Homo sapiens

US-08-927-939-21

Query Match 100.0%; Score 478; DB 13; Length 91;

Best Local Similarity 100.0%; Pred. No. 2.9e-46;

Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKVSAARLAVILIATLALCAPASAPYSSDTPCCFAYIARPLPRAHIKEYFTSGKCSNP 60  
|||||

Db 1 MKVSAARLAVILIATLALCAPASAPYSSDTPCCFAYIARPLPRAHIKEYFTSGKCSNP 60  
|||||

QY 61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91  
|||||

Db 61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91  
|||||

```
SULT 7
-08-927-939A-21
Sequence 21, Application US/08927939A
GENERAL INFORMATION:
APPLICANT: Grainger, David J.
APPLICANT: Tatalick, Lauren Marie
TITLE OF INVENTION: Compounds and methods to inhibit or
TITLE OF INVENTION: augment an inflammatory response.
FILE REFERENCE: 1543.001US1
CURRENT APPLICATION NUMBER: US/08/927,939A
CURRENT FILING DATE: 1997-11-09
NUMBER OF SEQ ID NOS: 85
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 21
LENGTH: 91
TYPE: PRT
ORGANISM: Homo sapiens
-08-927-939A-21

Query Match      100.0%; Score 478; DB 13; Length 91;
Best Local Similarity 100.0%; Pred. No. 2.9e-46;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKVSAARLAVILIATALCAPASAPYSSDTPCCPAYIARPLPRAHIKEYFYTSKCSNP 60
|||||
1 MKVSAARLAVILIATALCAPASAPYSSDTPCCPAYIARPLPRAHIKEYFYTSKCSNP 60
|||||
61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91
|||||
61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91
|||||

RESULT 9
US-09-113-705-8
; Sequence 8, Application US/09113705
; GENERAL INFORMATION:
; APPLICANT: BANDMAN, OLGA
; APPLICANT: COLEMAN, ROGER
; APPLICANT: STUART, SUSAN G.
; TITLE OF INVENTION: NEW CHEMOKINE EXPRESSED IN EOSINOPHILS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/113,705
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/421,144
; FILING DATE: 13-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Luther, Barbara J.
; REGISTRATION NUMBER: 33954
; REFERENCE/DOCKET NUMBER: PF-0031 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-852-0195
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 91 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-113-705-8

Query Match      100.0%; Score 478; DB 15; Length 91;
Best Local Similarity 100.0%; Pred. No. 2.9e-46;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKVSAARLAVILIATALCAPASAPYSSDTPCCPAYIARPLPRAHIKEYFYTSKCSNP 60
|||||
1 MKVSAARLAVILIATALCAPASAPYSSDTPCCPAYIARPLPRAHIKEYFYTSKCSNP 60
|||||
61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91
|||||
61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91
|||||

RESULT 10
US-09-023-092-4
Sequence 4, Application US/09023092
GENERAL INFORMATION:
APPLICANT: Hedrick, Joseph A.
APPLICANT: Wang, Luquan
APPLICANT: Zlotnik, Albert
APPLICANT: Murgolo, Nicholas J.
APPLICANT: Greene, Jonathan R.
TITLE OF INVENTION: Mammalian Chemokines; Related Reagents
TITLE OF INVENTION: and Methods
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,092
FILING DATE: 13-FEB-1998
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0780
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1200
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 91 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
```

ESULT 12  
S-09-150-813-21  
Sequence 21, Application US/09150813

RESULT 13  
US-09-208-803-12  
; Sequence 12, Application US/092080803  
; GENERAL INFORMATION:  
; APPLICANT: Wilde, Craig G.  
; APPLICANT: Hawkins, Phillip R.  
; APPLICANT: Bandman, Olga  
; APPLICANT: Seilhamer, Jeffrey J.  
; TITLE OF INVENTION: EXPRESSED CHEMOKINES, THEIR  
; TITLE OF INVENTION: PRODUCTION AND USES  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: U.S.  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/208,803  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/798,143  
; FILING DATE: 10-FEB-1997  
; APPLICATION NUMBER: 08/347,492  
; FILING DATE: 29-NOV-1994  
; APPLICATION NUMBER: 08/303,241  
; FILING DATE: 07-SEP-1994  
; APPLICATION NUMBER: 08/320,011  
; FILING DATE: 05-OCT-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Luther, Barbara J  
; REGISTRATION NUMBER: 33,954  
; REFERENCE/DOCKET NUMBER: PF-0024  
; TELECOMMUNICATION INFORMATION:



us-09-920-137a-8.rapm

Dec 16 15:54:10 2003

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/387,620  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/467,123  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0026-1 DIV  
TELEPHONE: 415-555-0555  
TELEFAX: 415-845-4166  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 91 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-387-620-5

Query Match 100.0%; Score 478; DB 16; Length 91;  
Best Local Similarity 100.0%; Pred. No. 2.9e-46;  
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 MKVSAARLAVILIALTALCAPASAPYSSDTPCCFAYIARPLPRAHIKEYFYTSKGKCSNP 60  
1 MKVSAARLAVILIALTALCAPASAPYSSDTPCCFAYIARPLPRAHIKEYFYTSKGKCSNP 60  
61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91  
61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91

Sequence 5, Application US/09360290  
GENERAL INFORMATION:  
APPLICANT: Bandman, Olga  
APPLICANT: Coleman, Roger  
APPLICANT: Stuart, Susan G.  
TITLE OF INVENTION: NEW CHEMOKINE EXPRESSED IN EOSINOPHILS  
FILE REFERENCE: PF-0031-2 DIV  
CURRENT APPLICATION NUMBER: US/09/360,290  
CURRENT FILING DATE: 1999-07-22  
EARLIER APPLICATION NUMBER: 08/421,144  
EARLIER FILING DATE: 1995-04-13  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: FastSEQ Version 3.0  
SEQ ID NO 5  
LENGTH: 91  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: Rantes  
09-360-290-5

Query Match 100.0%; Score 478; DB 17; Length 91;  
Best Local Similarity 100.0%; Pred. No. 2.9e-46;  
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 MKVSAARLAVILIALTALCAPASAPYSSDTPCCFAYIARPLPRAHIKEYFYTSKGKCSNP 60  
1 MKVSAARLAVILIALTALCAPASAPYSSDTPCCFAYIARPLPRAHIKEYFYTSKGKCSNP 60  
61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91  
61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91

Sequence 5, Application US/09387620  
GENERAL INFORMATION:  
APPLICANT: Coleman, Roger  
APPLICANT: Wilde, Craig C.  
APPLICANT: Seilhamer, Jeffrey J.  
TITLE OF INVENTION: CHEMOKINE EXPRESSED IN FETAL SPLEEN,  
ITS PRODUCTION AND USES  
NUMBER OF SEQUENCES: 9

Query Match 100.0%; Score 478; DB 17; Length 91;  
Best Local Similarity 100.0%; Pred. No. 2.9e-46;  
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 MKVSAARLAVILIALTALCAPASAPYSSDTPCCFAYIARPLPRAHIKEYFYTSKGKCSNP 60  
1 MKVSAARLAVILIALTALCAPASAPYSSDTPCCFAYIARPLPRAHIKEYFYTSKGKCSNP 60  
61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91  
61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91

Search completed: December 16, 2003, 15:46:43  
Job time : 165.59 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

protein - protein search, using sw model

on: December 16, 2003, 15:38:25 ; Search time 13.4262 Seconds  
(without alignments)  
366.280 Million cell updates/sec

le: US-09-920-137A-8  
fect score: 478  
quence: 1 MKVSAARLAVILIATLALCAP.....VCANPEKKWVREINSLMS 91

ring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

arched: 285895 seqs, 54041359 residues

al number of hits satisfying chosen parameters: 285895

imum DB seq length: 0  
imum DB seq length: 2000000000

st-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

abase : Pending Patents AA New: \*  
1: /cgn2\_6/ptodata/2/paa/pct NEW COMB.pep: \*  
2: /cgn2\_6/ptodata/2/paa/US06\_NEW COMB.pep: \*  
3: /cgn2\_6/ptodata/2/paa/US07\_NEW COMB.pep: \*  
4: /cgn2\_6/ptodata/2/paa/US08\_NEW COMB.pep: \*  
5: /cgn2\_6/ptodata/2/paa/US09\_NEW COMB.pep: \*  
6: /cgn2\_6/ptodata/2/paa/US10\_NEW COMB.pep: \*  
7: /cgn2\_6/ptodata/2/paa/US60\_NEW COMB.pep: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

sult No.	Score	Query Match	Length	DB ID	Description
1	472	98.7	91	6	US-10-398-457-1
2	472	98.7	91	7	US-60-487-610-2474
3	472	98.7	91	7	US-60-485-450-1561
4	466	97.5	91	6	US-10-398-457-8
5	466	97.5	91	6	US-10-398-457-9
6	466	97.5	91	6	US-10-398-457-10
7	466	97.5	91	6	US-10-398-457-11
8	466	97.5	91	6	US-10-398-457-12
9	466	97.5	91	6	US-10-398-457-13
10	454	95.0	91	6	US-10-398-457-3
11	454	95.0	91	6	US-10-398-457-6
12	443.5	92.8	92	6	US-10-398-457-7
13	374	78.2	68	1	PCT-US03-28745-4
14	374	78.2	68	6	US-10-622-134-11
15	374	78.2	68	6	US-10-332-038A-2
16	345	72.2	66	6	US-10-398-457-2
17	248	51.9	92	1	PCT-US03-21703-42
18	247	51.7	92	7	US-60-487-610-1678
19	247	51.7	92	7	US-60-485-450-1058
20	242.5	50.7	92	7	US-60-487-610-1677
21	242.5	50.7	92	7	US-60-485-450-1051
22	242.5	50.7	92	7	US-60-485-450-1057
23	242.5	50.7	92	7	US-60-485-450-1057
24	199.5	41.7	69	1	PCT-US03-28745-3
25	199.5	41.7	69	6	US-10-622-134-9
26	199.5	41.7	69	6	US-10-332-038A-9

27	199.5	41.7	70	6	US-10-332-038A-8	Sequence 8, Appli
28	199.5	41.7	70	6	US-10-398-457-31	Sequence 31, Appl
29	198.5	41.5	68	6	US-10-622-134-10	Sequence 10, Appl
30	190.5	39.9	69	6	US-10-398-457-5	Sequence 5, Appli
31	186	38.9	33	1	PCT-US03-28745-885	Sequence 885, App
32	186	38.9	33	1	PCT-US03-28745-930	Sequence 930, App
33	186	38.9	93	6	US-10-474-794-277	Sequence 277, App
34	186	38.9	93	6	US-10-474-794-279	Sequence 279, App
35	186	38.9	93	6	US-10-474-794-281	Sequence 281, App
36	186	38.9	93	7	US-60-487-610-2476	Sequence 2476, Ap
37	184.5	38.6	70	6	US-10-398-457-4	Sequence 4, Appli
38	182.5	38.2	89	7	US-60-487-610-2330	Sequence 2330, Ap
39	177.5	37.1	100	1	PCT-US03-28227-4411	Sequence 4411, Ap
40	174.5	36.5	94	7	US-60-487-610-2730	Sequence 2730, Ap
41	172	36.0	74	6	US-10-332-038A-15	Sequence 15, Appl
42	172	36.0	74	6	US-10-398-457-35	Sequence 35, Appl
43	167	34.9	99	1	PCT-US03-21703-41	Sequence 41, Appl
44	167	34.9	99	6	US-10-646-770-18	Sequence 18, Appl
45	165.5	34.6	120	7	US-60-487-610-2473	Sequence 2473, Ap

ALIGNMENTS

RESULT 1  
US-10-398-457-1  
; Sequence 1, Application US/10398457  
; GENERAL INFORMATION:  
; APPLICANT: APPLIED RESEARCH SYSTEMS ARS HOLDING N.V.  
; TITLE OF INVENTION: CHEMOKINES MUTANTS IN THE TREATMENT OF MULTIPLE SCLEROSIS  
; FILE REFERENCE: WO465  
; CURRENT APPLICATION NUMBER: US/10/398,457  
; CURRENT FILING DATE: 2003-11-13  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 91  
; TYPE: PRT  
; ORGANISM: Escherichia coli  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: (1)..(23)  
US-10-398-457-1

Query Match 98.7%; Score 472; DB 6; Length 91;  
Best Local Similarity 98.9%; Pred. No. 6.4e-46;  
Matches 90; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	MKVSAARLAVILIATLALCAPASAPSYSSDTPCCCFAYIARPLPRAHIKEYFTYSGKCSNP	60
Db	1	MKVSAARLAVILIATLALCAPASAPSYSSDTPCCCFAYIARPLPRAHIKEYFTYSGKCSNP	60
QY	61	AVVFVTRKNRQVCANPEKKWVREINSLMS	91
Db	61	AVVFVTRKNRQVCANPEKKWVREINSLMS	91

RESULT 2  
US-60-487-610-2474  
; Sequence 2474, Application US/60487610  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele  
; APPLICANT: HUANG, Hongjin  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,  
; TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001469  
; CURRENT APPLICATION NUMBER: US/60/487,610  
; CURRENT FILING DATE: 2003-07-17  
; NUMBER OF SEQ ID NOS: 97101  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2474  
; LENGTH: 91

TYPE: PRT  
ORGANISM: Homo sapiens  
-60-487-610-2474

Query Match 98.7%; Score 472; DB 7; Length 91;  
Best Local Similarity 98.9%; Pred. No. 6.4e-46;  
Matches 90; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 MKVSAARLAVILIATLALCAPASAPSYSSDTPCCFAYIARPLPRAHIKEYFYTSKGKCSNP 60  
1 MKVSAALAVILIATLALCAPASAPSYSSDTPCCFAYIARPLPRAHIKEYFYTSKGKCSNP 60

61 AVFVTRKNRQVCANPEKKWVREYINSLEMS 91  
61 AVFVTRKNRQVCANPEKKWVREYINSLEMS 91

SULT 3  
-60-485-450-1561  
Sequence 1561, Application US/60485450  
GENERAL INFORMATION:  
APPLICANT: CARGILL, Michele  
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C  
TITLE OF INVENTION: VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES  
TITLE OF INVENTION: THEREOF  
FILE REFERENCE: CL001470  
CURRENT APPLICATION NUMBER: US/60/485,450  
CURRENT FILING DATE: 2003-07-09  
NUMBER OF SEQ ID NOS: 47859  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1561  
LENGTH: 91  
TYPE: PRT  
ORGANISM: Homo sapiens  
-60-485-450-1561

Query Match 98.7%; Score 472; DB 7; Length 91;  
Best Local Similarity 98.9%; Pred. No. 6.4e-46;  
Matches 90; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 MKVSAARLAVILIATLALCAPASAPSYSSDTPCCFAYIARPLPRAHIKEYFYTSKGKCSNP 60  
1 MKVSAALAVILIATLALCAPASAPSYSSDTPCCFAYIARPLPRAHIKEYFYTSKGKCSNP 60

61 AVFVTRKNRQVCANPEKKWVREYINSLEMS 91  
61 AVFVTRKNRQVCANPEKKWVREYINSLEMS 91

RESULT 4  
-10-398-457-8  
Sequence 8, Application US/10398457  
GENERAL INFORMATION:  
APPLICANT: APPLIED RESEARCH SYSTEMS ARS HOLDING N.V.  
TITLE OF INVENTION: CHEMOKINES MUTANTS IN THE TREATMENT OF MULTIPLE SCLEROSIS  
FILE REFERENCE: WO465  
CURRENT APPLICATION NUMBER: US/10/398,457  
CURRENT FILING DATE: 2003-11-13  
NUMBER OF SEQ ID NOS: 37  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 8  
LENGTH: 91  
TYPE: PRT  
ORGANISM: Escherichia coli  
FEATURE:  
NAME/KEY: SIGNAL  
LOCATION: (1)..(23)  
-10-398-457-8

Query Match 97.5%; Score 466; DB 6; Length 91;  
Best Local Similarity 97.8%; Pred. No. 3e-45;

Matches 89; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MKVSAARLAVILIATLALCAPASAPSYSSDTPCCFAYIARPLPRAHIKEYFYTSKGKCSNP 60  
Db 1 MKVSAALAVILIATLALCAPASAPSYSSDTPCCFAYIARPLPRAHIKEYFYTSKGKCSNP 60

QY 61 AVFVTRKNRQVCANPEKKWVREYINSLEMS 91  
Db 61 AVFVTRKNRQVCANPEKKWVREYINSLEMS 91

RESULT 5  
US-10-398-457-9  
Sequence 9, Application US/10398457  
GENERAL INFORMATION:  
APPLICANT: APPLIED RESEARCH SYSTEMS ARS HOLDING N.V.  
TITLE OF INVENTION: CHEMOKINES MUTANTS IN THE TREATMENT OF MULTIPLE SCLEROSIS  
FILE REFERENCE: WO465  
CURRENT APPLICATION NUMBER: US/10/398,457  
CURRENT FILING DATE: 2003-11-13  
NUMBER OF SEQ ID NOS: 37  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 9  
LENGTH: 91  
TYPE: PRT  
ORGANISM: Escherichia coli  
FEATURE:  
NAME/KEY: SIGNAL  
LOCATION: (1)..(23)  
US-10-398-457-9

Query Match 97.5%; Score 466; DB 6; Length 91;  
Best Local Similarity 97.8%; Pred. No. 3e-45;  
Matches 89; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MKVSAARLAVILIATLALCAPASAPSYSSDTPCCFAYIARPLPRAHIKEYFYTSKGKCSNP 60  
Db 1 MKVSAALAVILIATLALCAPASAPSYSSDTPCCFAYIARPLPRAHIKEYFYTSKGKCSNP 60

QY 61 AVFVTRKNRQVCANPEKKWVREYINSLEMS 91  
Db 61 AVFVTRKNRQVCANPEKKWVREYINSLEMS 91

RESULT 6  
US-10-398-457-10  
Sequence 10, Application US/10398457  
GENERAL INFORMATION:  
APPLICANT: APPLIED RESEARCH SYSTEMS ARS HOLDING N.V.  
TITLE OF INVENTION: CHEMOKINES MUTANTS IN THE TREATMENT OF MULTIPLE SCLEROSIS  
FILE REFERENCE: WO465  
CURRENT APPLICATION NUMBER: US/10/398,457  
CURRENT FILING DATE: 2003-11-13  
NUMBER OF SEQ ID NOS: 37  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 10  
LENGTH: 91  
TYPE: PRT  
ORGANISM: Escherichia coli  
FEATURE:  
NAME/KEY: SIGNAL  
LOCATION: (1)..(23)  
US-10-398-457-10

Query Match 97.5%; Score 466; DB 6; Length 91;  
Best Local Similarity 97.8%; Pred. No. 3e-45;  
Matches 89; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MKVSAARLAVILIATLALCAPASAPSYSSDTPCCFAYIARPLPRAHIKEYFYTSKGKCSNP 60  
Db 1 MKVSAALAVILIATLALCAPASAPSYSSDTPCCFAYIARPLPRAHIKEYFYTSKGKCSNP 60

QY 61 AVFVTRKNRQVCANPEKKWVREYINSLEMS 91

|||||  
61 AVVFVTRKNQVCANPEKKWVREYINSLEMS 91

RESULT 7  
US-10-398-457-11  
Sequence 11, Application US/10398457  
GENERAL INFORMATION:  
APPLICANT: APPLIED RESEARCH SYSTEMS ARS HOLDING N.V.  
TITLE OF INVENTION: CHEMOKINES MUTANTS IN THE TREATMENT OF MULTIPLE SCLEROSIS  
FILE REFERENCE: WO465  
CURRENT APPLICATION NUMBER: US/10/398,457  
CURRENT FILING DATE: 2003-11-13  
NUMBER OF SEQ ID NOS: 37  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 11  
LENGTH: 91  
TYPE: PRT  
ORGANISM: Escherichia coli  
FEATURE:  
NAME/KEY: SIGNAL  
LOCATION: (1)..(23)  
US-10-398-457-11

Query Match 97.5%; Score 466; DB 6; Length 91;  
Best Local Similarity 97.8%; Pred. No. 3e-45;  
Matches 89; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 MKVSAARLAVILIATATCAPASASPYSSDTPCCFAYIARPLPRAHIKEYFTSGKCSNP 60  
Db 1 MKVSAALAVILIATATCAPASASPYSSDTPCCFAYIARPLPRAHIKEYFTSGKCSNP 60  
QY 61 AVVFVTRKNQVCANPEKKWVREYINSLEMS 91  
Db 61 AVVFVTRKNQVCANPEAKWVREYINSLEMS 91

RESULT 8  
US-10-398-457-12  
Sequence 12, Application US/10398457  
GENERAL INFORMATION:  
APPLICANT: APPLIED RESEARCH SYSTEMS ARS HOLDING N.V.  
TITLE OF INVENTION: CHEMOKINES MUTANTS IN THE TREATMENT OF MULTIPLE SCLEROSIS  
FILE REFERENCE: WO465  
CURRENT APPLICATION NUMBER: US/10/398,457  
CURRENT FILING DATE: 2003-11-13  
NUMBER OF SEQ ID NOS: 37  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 12  
LENGTH: 91  
TYPE: PRT  
ORGANISM: Escherichia coli  
FEATURE:  
NAME/KEY: SIGNAL  
LOCATION: (1)..(23)  
US-10-398-457-12

Query Match 97.5%; Score 466; DB 6; Length 91;  
Best Local Similarity 97.8%; Pred. No. 3e-45;  
Matches 89; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 MKVSAARLAVILIATATCAPASASPYSSDTPCCFAYIARPLPRAHIKEYFTSGKCSNP 60  
Db 1 MKVSAALAVILIATATCAPASASPYSSDTPCCFAYIARPLPRAHIKEYFTSGKCSNP 60  
QY 61 AVVFVTRKNQVCANPEKKWVREYINSLEMS 91  
Db 61 AVVFVTRKNQVCANPEKAWVREYINSLEMS 91

RESULT 9  
US-10-398-457-13  
Sequence 13, Application US/10398457

GENERAL INFORMATION:  
APPLICANT: APPLIED RESEARCH SYSTEMS ARS HOLDING N.V.  
TITLE OF INVENTION: CHEMOKINES MUTANTS IN THE TREATMENT OF MULTIPLE SCLEROSIS  
FILE REFERENCE: WO465  
CURRENT APPLICATION NUMBER: US/10/398,457  
CURRENT FILING DATE: 2003-11-13  
NUMBER OF SEQ ID NOS: 37  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 13  
LENGTH: 91  
TYPE: PRT  
ORGANISM: Escherichia coli  
FEATURE:  
NAME/KEY: SIGNAL  
LOCATION: (1)..(23)  
US-10-398-457-13

Query Match 97.5%; Score 466; DB 6; Length 91;  
Best Local Similarity 97.8%; Pred. No. 3e-45;  
Matches 89; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 MKVSAARLAVILIATATCAPASASPYSSDTPCCFAYIARPLPRAHIKEYFTSGKCSNP 60  
Db 1 MKVSAALAVILIATATCAPASASPYSSDTPCCFAYIARPLPRAHIKEYFTSGKCSNP 60  
QY 61 AVVFVTRKNQVCANPEKKWVREYINSLEMS 91  
Db 61 AVVFVTRKNQVCANPEKKWVAEYINSLEMS 91

RESULT 10  
US-10-398-457-3  
Sequence 3, Application US/10398457  
GENERAL INFORMATION:  
APPLICANT: APPLIED RESEARCH SYSTEMS ARS HOLDING N.V.  
TITLE OF INVENTION: CHEMOKINES MUTANTS IN THE TREATMENT OF MULTIPLE SCLEROSIS  
FILE REFERENCE: WO465  
CURRENT APPLICATION NUMBER: US/10/398,457  
CURRENT FILING DATE: 2003-11-13  
NUMBER OF SEQ ID NOS: 37  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 3  
LENGTH: 91  
TYPE: PRT  
ORGANISM: Escherichia coli  
FEATURE:  
NAME/KEY: SIGNAL  
LOCATION: (1)..(23)  
US-10-398-457-3

Query Match 95.0%; Score 454; DB 6; Length 91;  
Best Local Similarity 95.6%; Pred. No. 6.7e-44;  
Matches 87; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1 MKVSAARLAVILIATATCAPASASPYSSDTPCCFAYIARPLPRAHIKEYFTSGKCSNP 60  
Db 1 MKVSAALAVILIATATCAPASASPYSSDTPCCFAYIARPLPRAHIKEYFTSGKCSNP 60  
QY 61 AVVFVTRKNQVCANPEKKWVREYINSLEMS 91  
Db 61 AVVFVTAANAQVCANPEKKWVREYINSLEMS 91

RESULT 11  
US-10-398-457-6  
Sequence 6, Application US/10398457  
GENERAL INFORMATION:  
APPLICANT: APPLIED RESEARCH SYSTEMS ARS HOLDING N.V.  
TITLE OF INVENTION: CHEMOKINES MUTANTS IN THE TREATMENT OF MULTIPLE SCLEROSIS  
FILE REFERENCE: WO465  
CURRENT APPLICATION NUMBER: US/10/398,457  
CURRENT FILING DATE: 2003-11-13  
NUMBER OF SEQ ID NOS: 37



us-09-920-137a-8.rapn

Dec 16 15:54:10 2003

ARE: PatentIn version 3.0

NO 6  
TH: 91

ANISM: Escherichia coli

URE: SIGNAL

ATION: (1)..(23)

98-457-6

Match 95.0%; Score 454; DB 6; Length 91;  
Local Similarity 95.6%; Pred. No. 6.7e-44;  
es 87; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

1 MKVSAARLAVILIATLALCAPASASPYSSDTPCCFAYIARPLPRAHIKEYFYTSKGKCSNP 60

1 MKVSAALAVILIATLALCAPASASPYSSDTPCCFAYIARPLPRAHIKEYFYTSKGKCSNP 60

61 AVFVTRKNRQVCANPEKKWVREYINSLEMS 91

61 AVFVTRKNRQVCANPEKKWVREYINSLEMS 91

61 AVFVTRKNRQVCANPEKKWVREYINSLEMS 91

398-457-7

ence 7, Application US/10398457

AL INFORMATION: APPLIED RESEARCH SYSTEMS ARS HOLDING N.V.

PLICANT: CHEMOKINES MUTANTS IN THE TREATMENT OF MULTIPLE SCLEROSIS

LE OF INVENTION: CHEMOKINES MUTANTS IN THE TREATMENT OF MULTIPLE SCLEROSIS

LE REFERENCE: WO465

RRNT APPLICATION NUMBER: US/10/398,457

RRNT FILING DATE: 2003-11-13

MBER OF SEQ ID NOS: 37

FTWARE: PatentIn version 3.0

ID NO 7

LENGTH: 92

YPE: PRT

ORGANISM: Escherichia Coli

)-398-457-7

ery Match 92.8%; Score 443.5; DB 6; Length 92;

st Local Similarity 94.6%; Pred. No. 1e-42; Indels 4; Gaps 1;

tches 87; Conservative 0; Mismatches 4; Indels 4; Gaps 1;

1 MKVSAARLAVILIATLALCAPASA-SPYSSDTPCCFAYIARPLPRAHIKEYFYTSKGKCSN 59

1 MKVSAALAVILIATLALCAPASAMSPYSSDTPCCFAYIARPLPRAHIKEYFYTSKGKCSN 60

60 PAVFVTRKNRQVCANPEKKWVREYINSLEMS 91

61 PAVFVTAANAQVCANPEKKWVREYINSLEMS 92

ULT 13

-US03-28745-4

equence 4, Application PC/TUS0328745

GENERAL INFORMATION: APPLICATION: CHEMOKINE THERAPEUTICS CORP.

APPLICANT: CHEMOKINE THERAPEUTICS CORP.

TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES

FILE REFERENCE: 59296.00003

CURRENT APPLICATION NUMBER: PCT/US03/28745

CURRENT FILING DATE: 2003-09-11

NUMBER OF SEQ ID NOS: 1640

SOFTWARE: PatentIn version 3.2

SEQ ID NO 4

LENGTH: 68

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: Description of Artificial Sequence: Synthetic peptide

OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide

T-US03-28745-4

Query Match 78.2%; Score 374; DB 1; Length 68;

Best Local Similarity 100.0%; Pred. No. 4.5e-35; Indels 0; Gaps 0;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

24 SPYSSDTPCCFAYIARPLPRAHIKEYFYTSKGKCSNPVAVFVTRKNRQVCANPEKKWVRE 83

1 SPYSSDTPCCFAYIARPLPRAHIKEYFYTSKGKCSNPVAVFVTRKNRQVCANPEKKWVRE 60

84 YINSLEMS 91

61 YINSLEMS 68

84 YINSLEMS 91

61 YINSLEMS 68

RESULT 14

US-10-622-134-11

; Sequence 11, Application US/10622134

; GENERAL INFORMATION: APPLICANT: WILLIAMS, TIMOTHY J.

; APPLICANT: JOSE, PETER J.

; GRIFFITHS-JOHNSON, DAVID A.

; HSUAN, JOHN J.

; TITLE OF INVENTION: CHEMOTACTIC CYTOKINE

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS: ADDRESS: NIXON & VANDERHYE P.C.

; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR

; CITY: ARLINGTON

; STATE: VIRGINIA

; COUNTRY: U.S.A.

; ZIP: 22201-4714

; COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA: APPLICATION NUMBER: US/10/622,134

; FILING DATE: 18-Jul-2003

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA: APPLICATION NUMBER: US/09/291,038

; FILING DATE: 14-Apr-1999

; APPLICATION NUMBER: <Unknown>

; FILING DATE: <Unknown>

; APPLICATION NUMBER: US/08/615,232A

; FILING DATE: 13-AUG-1996

; APPLICATION NUMBER: GB 9318984

; FILING DATE: 14-SEP-1993

; APPLICATION NUMBER: GB 9408602

; FILING DATE: 29-APR-1994

; ATTORNEY/AGENT INFORMATION: NAME: WILSON, MARY J.

; REGISTRATION NUMBER: 32,955

; REFERENCE/DOCKET NUMBER: 550-32

; TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 816-4000

; TELEFAX: (703) 816-4100

; INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 68 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 11:

; US-10-622-134-11

Query Match 78.2%; Score 374; DB 6; Length 68;

Best Local Similarity 100.0%; Pred. No. 4.5e-35;

Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

24 SPYSSDTPCCFAYIARPLPRAHIKEYFYTSKGKCSNPVAVFVTRKNRQVCANPEKKWVRE 83

1 SPYSSDTPCCFAYIARPLPRAHIKEYFYTSKGKCSNPVAVFVTRKNRQVCANPEKKWVRE 60

QY

Db

84 YINSLEMS 91  
|||||  
61 YINSLEMS 68

SULT 15  
-10-332-038A-2  
Sequence 2, Application US/10332038A  
GENERAL INFORMATION:  
APPLICANT: Gryphon Therapeutics, Inc.  
APPLICANT: Offord, Robin  
APPLICANT: Gaertner, Hubert  
APPLICANT: Hartley, Oliver  
TITLE OF INVENTION: Chemokine Receptor Modulators, Production and Use  
FILE REFERENCE: 03504.271  
CURRENT APPLICATION NUMBER: US/10/332,038A  
CURRENT FILING DATE: 2003-05-06  
PRIOR APPLICATION NUMBER: US 60/217,683  
PRIOR FILING DATE: 2000-07-12  
NUMBER OF SEQ ID NOS: 28  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 2  
LENGTH: 68  
TYPE: PRT  
ORGANISM: Homo Sapiens  
-10-332-038A-2

Query Match 78.2%; Score 374; DB 6; Length 68;  
Best Local Similarity 100.0%; Pred. No. 4.5e-35;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
24 SPYSSDTPCCFAYIARPLPRAHIKEYFTSGKCSNPAAWVFVTRKNRQVCANPEKKWVRE 83  
1 SPYSSDTPCCFAYIARPLPRAHIKEYFTSGKCSNPAAWVFVTRKNRQVCANPEKKWVRE 60

84 YINSLEMS 91  
|||||  
61 YINSLEMS 68

arch completed: December 16, 2003, 15:47:23  
b time : 13.4262 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

1 protein - protein search, using sw model  
in on: December 16, 2003, 15:36:20 ; Search time 14.4208 Seconds  
(without alignments)  
266.996 Million cell updates/sec

itle: US-09-920-137A-8  
ffect score: 478  
equence: 1 MKVSAARLAVILIATLALCAP.....VCANPEKKVREYINSLEMS 91

oring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

arched: 328717 seqs, 42310858 residues

otal number of hits satisfying chosen parameters: 328717

inimum DB seq length: 0  
aximum DB seq length: 2000000000

ost-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

atabase : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	478	100.0	91	1	US-08-347-492B-12
2	478	100.0	91	1	US-08-375-346A-5
3	478	100.0	91	2	US-08-633-682-3
4	478	100.0	91	2	US-08-421-144A-8
5	478	100.0	91	2	US-08-798-143-12
6	478	100.0	91	2	US-08-467-123B-5
7	478	100.0	91	3	US-08-936-772-3
8	478	100.0	91	3	US-08-836-922-14
9	478	100.0	91	3	US-09-395-918-3
10	478	100.0	91	4	US-09-230-371A-25
11	478	100.0	91	4	US-09-639-881-14
12	472	98.7	91	1	US-08-480-449-21
13	472	98.7	91	2	US-08-660-542-21
14	472	98.7	91	4	US-08-679-493A-155
15	472	98.7	91	4	US-08-479-603-21
16	472	98.7	91	4	US-08-939-107-21
17	469	98.1	90	3	US-09-230-637-40
18	397	83.1	91	4	US-08-679-493A-156
19	393	82.2	91	2	US-08-633-682-5
20	393	82.2	91	3	US-08-936-772-5
21	393	82.2	91	3	US-09-395-918-5
22	374	78.2	68	2	US-08-936-387-1
23	374	78.2	68	2	US-08-615-232A-11
24	374	78.2	68	3	US-08-470-323-11
25	374	78.2	68	3	US-08-836-922-1
26	374	78.2	68	3	US-09-141-833-1
27	374	78.2	68	4	US-09-639-881-1

28	374	78.2	69	3	US-08-836-922-2	Sequence 2, Appli
29	374	78.2	69	3	US-08-836-922-3	Sequence 3, Appli
30	374	78.2	69	3	US-08-836-922-4	Sequence 4, Appli
31	374	78.2	69	4	US-09-639-881-2	Sequence 2, Appli
32	374	78.2	69	4	US-09-639-881-3	Sequence 3, Appli
33	374	78.2	69	4	US-09-639-881-4	Sequence 4, Appli
34	374	78.2	73	2	US-08-936-387-13	Sequence 13, Appl
35	374	78.2	76	3	US-08-836-922-20	Sequence 20, Appl
36	374	78.2	76	4	US-09-639-881-20	Sequence 20, Appl
37	370	77.4	67	3	US-09-141-833-2	Sequence 2, Appli
38	370	77.4	68	3	US-09-141-833-5	Sequence 5, Appli
39	369	77.2	68	2	US-08-936-387-17	Sequence 17, Appl
40	368	77.0	68	2	US-08-936-387-16	Sequence 16, Appl
41	366	76.6	68	2	US-08-716-188-5	Sequence 5, Appli
42	363	75.9	66	4	US-09-555-663-2	Sequence 2, Appli
43	363	75.9	68	2	US-08-936-387-18	Sequence 18, Appl
44	353	73.8	66	1	US-08-330-163-14	Sequence 14, Appl
45	353	73.8	66	1	US-08-482-111-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1  
US-08-347-492B-12  
; Sequence 12, Application US/08347492B  
; Patent No. 5602008  
; GENERAL INFORMATION:  
; APPLICANT: Wilde, Craig G.  
; APPLICANT: Hawkins, Phillip R.  
; APPLICANT: Bandman, Olga  
; APPLICANT: Seilhamer, Jeffrey J.  
; TITLE OF INVENTION: EXPRESSED CHEMOKINES, THEIR  
; PRODUCTION AND USES  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: U.S.  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/347,492B  
; FILING DATE: 29-NOV-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/303,241  
; FILING DATE: 07-SEP-1994  
; APPLICATION NUMBER: 08/320,011  
; FILING DATE: 05-OCT-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Luther, Barbara J  
; REGISTRATION NUMBER: 33,954  
; REFERENCE/DOCKET NUMBER: PF-0024  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-852-0195  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 91 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; IMMEDIATE SOURCE:  
; LIBRARY: GENBANK  
; CLONE: GI 134510  
US-08-347-492B-12

Query Match 100.0%; Score 478; DB 1; Length 91;  
Best Local Similarity 100.0%; Pred. No. 1e-47;  
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKVSAARLAVILIATLALCAPASAPYSSDTPCCFAYIARPLPRAHIKEYFYTSKGKSNP 60  
1 MKVSAARLAVILIATLALCAPASAPYSSDTPCCFAYIARPLPRAHIKEYFYTSKGKSNP 60

61 AVFVTRKNRQVCANPEKKWVREYINSLEMS 91  
61 AVFVTRKNRQVCANPEKKWVREYINSLEMS 91

RESULT 2  
US-08-375-346A-5  
Sequence 5, Application US/08375346A  
Patent No. 5605817  
GENERAL INFORMATION:  
APPLICANT: Coleman, Roger  
APPLICANT: Wilde, Craig G.  
APPLICANT: Seilhamer, Jeffrey J.  
TITLE OF INVENTION: A NEW CHEMOKINE EXPRESSED IN FETAL SPLEEN,  
TITLE OF INVENTION: ITS PRODUCTION AND USES  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3330 HILLVIEW AVENUE  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/375,346A  
FILING DATE: 19-JAN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: LUTHER, BARBARA J.  
REGISTRATION NUMBER: 33,954  
REFERENCE/DOCKET NUMBER: PF-0026 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 855-0555  
TELEFAX: (415) 855-0572  
TELEX:  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 91 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
S-08-375-346A-5

Query Match 100.0%; Score 478; DB 1; Length 91;  
Best Local Similarity 100.0%; Pred. No. 1e-47;  
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKVSAARLAVILIATLALCAPASAPYSSDTPCCFAYIARPLPRAHIKEYFYTSKGKSNP 60  
1 MKVSAARLAVILIATLALCAPASAPYSSDTPCCFAYIARPLPRAHIKEYFYTSKGKSNP 60

QY 61 AVFVTRKNRQVCANPEKKWVREYINSLEMS 91  
Db 61 AVFVTRKNRQVCANPEKKWVREYINSLEMS 91

RESULT 3  
US-08-633-682-3  
Sequence 3, Application US/08633682  
Patent No. 5840544  
GENERAL INFORMATION:  
APPLICANT: Hawkins, Phillip R.  
APPLICANT: Bandman, Olga  
APPLICANT: Murry, Lynn E.  
TITLE OF INVENTION: NOVEL RANTES HOMOLOG FROM PROSTATE  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/633,682  
FILING DATE: Filed Herewith  
ATTORNEY/AGENT INFORMATION:  
NAME: Luther, Barbara J  
REGISTRATION NUMBER: 33,954  
REFERENCE/DOCKET NUMBER: PF-0063 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-852-0195  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 91 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: GI 134510  
US-08-633-682-3

Query Match 100.0%; Score 478; DB 2; Length 91;  
Best Local Similarity 100.0%; Pred. No. 1e-47;  
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKVSAARLAVILIATLALCAPASAPYSSDTPCCFAYIARPLPRAHIKEYFYTSKGKSNP 60  
1 MKVSAARLAVILIATLALCAPASAPYSSDTPCCFAYIARPLPRAHIKEYFYTSKGKSNP 60

61 AVFVTRKNRQVCANPEKKWVREYINSLEMS 91  
61 AVFVTRKNRQVCANPEKKWVREYINSLEMS 91

RESULT 4  
US-08-421-144A-8  
Sequence 8, Application US/08421144A  
Patent No. 5874211  
GENERAL INFORMATION:  
APPLICANT: BANDMAN, OLGA  
APPLICANT: COLEMAN, ROGER  
APPLICANT: STUART, SUSAN G.  
TITLE OF INVENTION: NEW CHEMOKINE EXPRESSED IN EOSINOPHILS  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:



ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/421,144A  
FILING DATE: 13-APR-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Luther, Barbara J.  
REGISTRATION NUMBER: 33954  
REFERENCE/DOCKET NUMBER: PF-0031 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-852-0195  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 91 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
-08-421-144A-8  
Query Match 100.0%; Score 478; DB 2; Length 91;  
Best Local Similarity 100.0%; Pred. No. 1e-47;  
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 MKVSAARLAVILIATLALCAPASAPSYSSDTPCCFAYIARPLPRAHIKEYFYTSKGKCSNP 60  
1 MKVSAARLAVILIATLALCAPASAPSYSSDTPCCFAYIARPLPRAHIKEYFYTSKGKCSNP 60  
61 AVFVTRKNRQVCANPEKKWVREYINSLEMS 91  
61 AVFVTRKNRQVCANPEKKWVREYINSLEMS 91  
RESULT 5  
1-08-798-143-12  
Sequence 12, Application US/08798143  
Patent No. 5936068  
GENERAL INFORMATION:  
APPLICANT: Wilde, Craig G.  
APPLICANT: Hawkins, Phillip R.  
APPLICANT: Bandman, Olga  
APPLICANT: Seilhamer, Jeffrey J.  
TITLE OF INVENTION: EXPRESSED CHEMOKINES, THEIR  
TITLE OF INVENTION: PRODUCTION AND USES  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/798,143  
FILING DATE: 10-FEB-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION INFORMATION:

APPLICATION NUMBER: 08/347,492  
FILING DATE: 29-NOV-1994  
APPLICATION NUMBER: 08/303,241  
FILING DATE: 07-SEP-1994  
APPLICATION NUMBER: 08/320,011  
FILING DATE: 05-OCT-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Luther, Barbara J.  
REGISTRATION NUMBER: 33,954  
REFERENCE/DOCKET NUMBER: PF-0024  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-852-0195  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 91 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
LIBRARY: GENBANK  
CLONE: GI 134510  
US-08-798-143-12  
Query Match 100.0%; Score 478; DB 2; Length 91;  
Best Local Similarity 100.0%; Pred. No. 1e-47;  
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKVSAARLAVILIATLALCAPASAPSYSSDTPCCFAYIARPLPRAHIKEYFYTSKGKCSNP 60  
Db 1 MKVSAARLAVILIATLALCAPASAPSYSSDTPCCFAYIARPLPRAHIKEYFYTSKGKCSNP 60  
QY 61 AVFVTRKNRQVCANPEKKWVREYINSLEMS 91  
Db 61 AVFVTRKNRQVCANPEKKWVREYINSLEMS 91  
RESULT 6  
US-08-467-123B-5  
Sequence 5, Application US/08467123B  
Patent No. 5945506  
GENERAL INFORMATION:  
APPLICANT: Coleman, Roger  
APPLICANT: Wilde, Craig C.  
APPLICANT: Seilhamer, Jeffrey J.  
TITLE OF INVENTION: CHEMOKINE EXPRESSED IN FETAL SPLEEN,  
TITLE OF INVENTION: ITS PRODUCTION AND USES  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,123B  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/375,346  
FILING DATE: 19-JAN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0026-1 DIV  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-555-0555  
TELEFAX: 415-845-4166  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 91 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
-08-467-123B-5

Query Match 100.0%; Score 478; DB 2; Length 91;  
Best Local Similarity 100.0%; Pred. No. 1e-47;  
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
1 MKVSAARLAVILIATLALCAPASAPYSSDTPCCCFAYIARPLPRAHIKEYFTSGKCSNP 60  
|||||  
1 MKVSAARLAVILIATLALCAPASAPYSSDTPCCCFAYIARPLPRAHIKEYFTSGKCSNP 60  
|||||  
  
61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91  
|||||  
61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91  
|||||

SULT 7  
-08-936-772-3  
Sequence 3, Application US/08936772  
Patent No. 6015883  
GENERAL INFORMATION:  
APPLICANT: Hawkins, Phillip R.  
APPLICANT: Bandman, Olga  
APPLICANT: Murry, Lynn E.  
TITLE OF INVENTION: NOVEL RANTES HOMOLOG FROM PROSTATE  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.  
ZIP: 94304

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/936,772  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/633,682  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Luther, Barbara J  
REGISTRATION NUMBER: 33,954  
REFERENCE/DOCKET NUMBER: PF-0063 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-852-0195  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 91 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: GI 134510  
S-08-936-772-3

Query Match 100.0%; Score 478; DB 3; Length 91;  
Best Local Similarity 100.0%; Pred. No. 1e-47;

Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MKVSAARLAVILIATLALCAPASAPYSSDTPCCCFAYIARPLPRAHIKEYFTSGKCSNP 60  
|||||  
Db 1 MKVSAARLAVILIATLALCAPASAPYSSDTPCCCFAYIARPLPRAHIKEYFTSGKCSNP 60  
|||||  
  
QY 61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91  
|||||  
Db 61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91  
|||||

RESULT 8  
US-08-836-922-14  
Sequence 14, Application US/08836922  
Patent No. 6159711  
GENERAL INFORMATION:  
APPLICANT: INNES PROUDFOOT, AMANDA ELIZABETH  
APPLICANT: WELLS, TIMOTHY NIGEL CARL  
TITLE OF INVENTION: RANTES PEPTIDE AND FRAGMENTS AND  
TITLE OF INVENTION: COMPOSITIONS COMPRISING IT FOR TREATMENT OF INFLAMMATION  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHVE P.C.  
STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/836,922  
FILING DATE: 23-MAY-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9424835.8  
FILING DATE: 08-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: WILSON, MARY J.  
REGISTRATION NUMBER: 32,955  
REFERENCE/DOCKET NUMBER: 1430-163  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 816-4011  
TELEFAX: (703) 816-4100  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 91 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-836-922-14

Query Match 100.0%; Score 478; DB 3; Length 91;  
Best Local Similarity 100.0%; Pred. No. 1e-47;  
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MKVSAARLAVILIATLALCAPASAPYSSDTPCCCFAYIARPLPRAHIKEYFTSGKCSNP 60  
|||||  
Db 1 MKVSAARLAVILIATLALCAPASAPYSSDTPCCCFAYIARPLPRAHIKEYFTSGKCSNP 60  
|||||  
  
QY 61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91  
|||||  
Db 61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91  
|||||

RESULT 9  
US-09-395-918-3

```
Sequence 3, Application US/09395918
Patent No. 6238666
GENERAL INFORMATION:
  APPLICANT: Hawkins, Phillip R.
  APPLICANT: Bandman, Olga
  APPLICANT: Murry, Lynn E.
  TITLE OF INVENTION: DNA ENCODING RANTES HOMOLOG FROM PROSTATE
  FILE REFERENCE: PF-0063 US
  CURRENT APPLICATION NUMBER: US/09/395,918
  CURRENT FILING DATE: 1999-09-14
  NUMBER OF SEQ ID NOS: 5
  SOFTWARE: PERL Program
SEQ ID NO 3
  LENGTH: 91
  TYPE: PRT
  ORGANISM: Homo sapiens
  FEATURE:
  NAME/KEY: misc feature
  OTHER INFORMATION: GenBank: GI 134510
;-09-395-918-3

Query Match          100.0%; Score 478; DB 3; Length 91;
Best Local Similarity 100.0%; Pred. No. 1e-47;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKVSAARLAVILIATALCAPASASPYSDDTTPCCFAYIARPLPRAHIKEYFTSGKCSNP 60
|||||
1 MKVSAARLAVILIATALCAPASASPYSDDTTPCCFAYIARPLPRAHIKEYFTSGKCSNP 60

61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91
|||||
61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91

RESULT 10
;-09-230-371A-25
Sequence 25, Application US/09230371A
Patent No. 6348586
GENERAL INFORMATION:
  APPLICANT: Chang, Yuan
  APPLICANT: Bohenzky, Roy A
  APPLICANT: Russo, James J
  APPLICANT: Edelman, Isidore S
  APPLICANT: Moore, Patrick S
  TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS SEQUENCES AND
  TITLE OF INVENTION: USES THEREOF
  FILE REFERENCE: 45185-G-PCT-US
  CURRENT APPLICATION NUMBER: US/09/230,371A
  CURRENT FILING DATE: 1999-11-17
  PRIOR APPLICATION NUMBER: PCT/US97/13346
  PRIOR FILING DATE: 1997-07-22
  NUMBER OF SEQ ID NOS: 30
  SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 25
  LENGTH: 91
  TYPE: PRT
  ORGANISM: Human
S-09-230-371A-25

Query Match          100.0%; Score 478; DB 4; Length 91;
Best Local Similarity 100.0%; Pred. No. 1e-47;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKVSAARLAVILIATALCAPASASPYSDDTTPCCFAYIARPLPRAHIKEYFTSGKCSNP 60
|||||
1 MKVSAARLAVILIATALCAPASASPYSDDTTPCCFAYIARPLPRAHIKEYFTSGKCSNP 60

61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91
|||||
61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91

Sequence 14, Application US/09639881
Patent No. 6555105
GENERAL INFORMATION:
  APPLICANT: INNES PROUDFOOT, AMANDA ELIZABETH
  APPLICANT: WELLS, TIMOTHY NIGEL CARL
  TITLE OF INVENTION: RANTES PEPTIDE AND FRAGMENTS AND
  TITLE OF INVENTION: COMPOSITIONS COMPRISING IT FOR TREATMENT OF INFLAMMATION
  NUMBER OF SEQUENCES: 20
  CORRESPONDENCE ADDRESS:
  ADDRESSEE: NIXON & VANDERHYE P.C.
  STREET: 1100 NORTH GLEBE ROAD
  CITY: ARLINGTON
  STATE: VIRGINIA
  COUNTRY: U.S.A.
  ZIP: 22201-4714
  COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: PatentIn Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/639,881
  FILING DATE: 17-AUG-2000
  PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US/08/836,922
  FILING DATE: 23-MAY-1997
  PRIOR APPLICATION DATA:
  APPLICATION NUMBER: GB 9424835.8
  FILING DATE: 08-DEC-1994
  PRIOR APPLICATION DATA:
  APPLICATION NUMBER: GB 9512319.6
  FILING DATE: 16-JUN-1995
  ATTORNEY/AGENT INFORMATION:
  NAME: WILSON, MARY J.
  REGISTRATION NUMBER: 32,955
  REFERENCE/DOCKET NUMBER: 1430-163
  TELECOMMUNICATION INFORMATION:
  TELEPHONE: (703) 816-4011
  TELEFAX: (703) 816-4100
  INFORMATION FOR SEQ ID NO: 14:
  SEQUENCE CHARACTERISTICS:
  LENGTH: 91 amino acids
  TYPE: amino acid
  TOPOLOGY: linear
  MOLECULE TYPE: protein
US-09-639-881-14

Query Match          100.0%; Score 478; DB 4; Length 91;
Best Local Similarity 100.0%; Pred. No. 1e-47;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKVSAARLAVILIATALCAPASASPYSDDTTPCCFAYIARPLPRAHIKEYFTSGKCSNP 60
|||||
1 MKVSAARLAVILIATALCAPASASPYSDDTTPCCFAYIARPLPRAHIKEYFTSGKCSNP 60

61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91
|||||
61 AVVFVTRKNRQVCANPEKKWVREYINSLEMS 91

RESULT 12
US-08-480-449-21
Sequence 21, Application US/08480449
Patent No. 5688927
GENERAL INFORMATION:
  APPLICANT: Godiska, Ronald
  APPLICANT: Gray, Patrick W.
  TITLE OF INVENTION: MACROPHAGE DERIVED CHEMOKINE
  NUMBER OF SEQUENCES: 24
  CORRESPONDENCE ADDRESS:
  ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
  STREET: 6300 Sears Tower, 233 South Wacker Drive
```

Tue Dec 16 15:54:10 2003

CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/480,449  
FILING DATE:  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Gass, David A.  
REGISTRATION NUMBER: 38,153  
REFERENCE/DOCKET NUMBER: 27866/32779  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 91 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: "RANTES"

3-08-480-449-21

Query Match 98.7%; Score 472; DB 1; Length 91;  
Best Local Similarity 98.9%; Pred. No. 5.1e-47;  
Matches 90; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 MKVSAARLAVILIATLALCAPASAPYSSDTPCCFAYIARPLPRAHIKEYFYTSKGKCSNP 60  
1 MKVSAALAVILIATLALCAPASAPYSSDTPCCFAYIARPLPRAHIKEYFYTSKGKCSNP 60  
61 AVFVTRKNQVCANPEKKWVREYINSLEMS 91  
61 AVFVTRKNQVCANPEKKWVREYINSLEMS 91

ESULT 13  
S-08-660-542-21  
Sequence 21, Application US/08660542  
Patent No. 5932703  
GENERAL INFORMATION:  
APPLICANT: Godiska, Ronald  
APPLICANT: Gray, Patrick W.  
TITLE OF INVENTION: MACROPHAGE DERIVED CHEMOKINE AND CHEMOKINE  
TITLE OF INVENTION: ANALOGS  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/660,542  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/558,658  
FILING DATE: 16-NOV-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/479,620  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Gass, David A.  
REGISTRATION NUMBER: 38,153  
REFERENCE/DOCKET NUMBER: 27866/33318  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 91 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: "RANTES"  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1.68  
US-08-660-542-21

Query Match 98.7%; Score 472; DB 2; Length 91;  
Best Local Similarity 98.9%; Pred. No. 5.1e-47;  
Matches 90; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 MKVSAARLAVILIATLALCAPASAPYSSDTPCCFAYIARPLPRAHIKEYFYTSKGKCSNP 60  
1 MKVSAALAVILIATLALCAPASAPYSSDTPCCFAYIARPLPRAHIKEYFYTSKGKCSNP 60  
61 AVFVTRKNQVCANPEKKWVREYINSLEMS 91  
61 AVFVTRKNQVCANPEKKWVREYINSLEMS 91

RESULT 14  
US-08-679-493A-155  
Sequence 155, Application US/08679493A  
Patent No. 6303295  
GENERAL INFORMATION:  
APPLICANT: Taylor, Ethan W.  
TITLE OF INVENTION: SELENOPTOGENS, CODING SEQUENCES AND METHODS  
FILE REFERENCE: 55-95  
CURRENT APPLICATION NUMBER: US/08/679,493A  
CURRENT FILING DATE: 1996-07-12  
PRIOR APPLICATION NUMBER: 60/001203  
PRIOR FILING DATE: 1995-07-14  
PRIOR APPLICATION NUMBER: 60/003,112  
PRIOR FILING DATE: 1995-09-01  
NUMBER OF SEQ ID NOS: 216  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 155  
LENGTH: 91  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-08-679-493A-155

Query Match 98.7%; Score 472; DB 4; Length 91;  
Best Local Similarity 98.9%; Pred. No. 5.1e-47;  
Matches 90; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 MKVSAARLAVILIATLALCAPASAPYSSDTPCCFAYIARPLPRAHIKEYFYTSKGKCSNP 60  
1 MKVSAALAVILIATLALCAPASAPYSSDTPCCFAYIARPLPRAHIKEYFYTSKGKCSNP 60  
61 AVFVTRKNQVCANPEKKWVREYINSLEMS 91



61 AVVFVTRKNQVCANPEKKWVREYINSLEMS 91

SULT 15

-08-479-603-21

Sequence 21, Application US/08479603

Patent No. 6320023

GENERAL INFORMATION:

APPLICANT: Godiska, Ronald

APPLICANT: Gray, Patrick W.

TITLE OF INVENTION: MACROPHAGE DERIVED CHEMOKINE

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: United States of America

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/479,603

FILING DATE:

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Gass, David A.

REGISTRATION NUMBER: 38,153

REFERENCE/DOCKET NUMBER: 27866/32780

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/474-6300

TELEFAX: 312/474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:

LENGTH: 91 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: misc feature

OTHER INFORMATION: "RANTES"

-08-479-603-21

Query Match 98.7%; Score 472; DB 4; Length 91;

Best Local Similarity 98.9%; Pred. No. 5.1e-47;

Matches 90; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 MKVSAARLAVILLIATLALCAPASASPYSSDTPCCFAYIARPLPRAHIKEYFYTSKGKSNP 60

|||||

1 MKVSAARLAVILLIATLALCAPASASPYSSDTPCCFAYIARPLPRAHIKEYFYTSKGKSNP 60

61 AVVFVTRKNQVCANPEKKWVREYINSLEMS 91

|||||

61 AVVFVTRKNQVCANPEKKWVREYINSLEMS 91

Search completed: December 16, 2003, 15:40:18

Search time: 15.4208 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

protein - protein search, using sw model

n on: December 16, 2003, 15:36:20 ; Search time 13.5738 Seconds  
(without alignments)  
651.810 Million cell updates/sec

tle: US-09-920-137A-7

rfect score: 486

quence: 1 MKLCVTVLSSLLMLVAAPFCSP.....VCADPSESWVQEVVYDLELN 92

oring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

arched: 283308 seqs, 96168682 residues

tal number of hits satisfying chosen parameters: 283308

nimum DB seq length: 0

ximum DB seq length: 2000000000

st-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

tabase : PIR 76:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	486	100.0	92	1 A31767	macrophage inflamm
2	409	84.2	92	2 I46730	immune activation
3	390	80.2	92	2 C30552	macrophage inflamm
4	320.5	65.9	92	2 A32393	macrophage inflamm
5	320	65.8	93	2 B35673	LD78-beta protein
6	303.5	62.4	92	2 I52322	macrophage inflamm
7	300.5	61.8	92	2 A30574	macrophage inflamm
8	263	54.1	50	2 C60407	monocyte adherence
9	245.5	50.5	91	1 A28815	monocyte chemoattr
10	242.5	49.9	91	1 A46539	monocyte chemoattr
11	197.5	40.6	148	1 S07723	immediate-early se
12	192.5	39.6	109	2 A54678	monocyte chemotact
13	185.5	38.2	148	1 A30209	PDGF-inducible JE
14	183.5	37.8	120	2 I48147	monocyte chemoattr
15	180.5	37.1	99	2 JC2136	monocyte chemoattr
16	178.5	36.7	97	2 JC4912	eotaxin precursor
17	174.5	35.9	125	2 I46857	monocyte chemoattr
18	172.5	35.5	99	1 A39296	monocyte chemoattr
19	172.5	35.5	99	2 JC2336	monocyte chemoattr
20	172.5	35.5	99	2 A60299	monocyte chemoattr
21	170.5	35.1	99	2 JC5295	monocyte chemotact
22	167.5	34.5	99	2 JC2417	monocyte chemoattr
23	167	34.4	120	2 JE0177	lymphocyte and mon
24	161	33.1	96	2 JC2478	eotaxin precursor
25	161	33.1	96	2 I48099	eotaxin precursor
26	141.5	29.1	97	2 A48093	monocytic cytokine
27	137.5	28.3	96	2 A37236	I-309 protein prec
28	131.5	27.1	116	2 I49555	gene C10 protein -
29	123.5	25.4	52	2 B60407	monocyte adherence

RESULT 1

A31767

macrophage inflammatory protein 1-beta precursor [validated] - human

N;Alternate names: cytokine HC21; G-26 protein; H400 homolog; lymphocyte activation ge

protein 2 (Act-2); T-cell activation protein gamma

C;Species: Homo sapiens (man)

C;Date: 07-Jun-1990 #sequence revision 29-May-1998 #text change 15-Sep-2000

C;Accession: JH0319; A40978; A31767; A37411; B30574; B45817; D30552

R;Baixeras, E.; Roman-Roman, S.; Jitsukawa, S.; Genevee, C.; Mechiche, S.; Viegas-Pegu

Mol. Immunol. 27, 1091-1102, 1990

A;Title: Cloning and expression of a lymphocyte activation gene (LAG-1).

A;Reference number: JH0319; MUID:91061800; PMID:2247088

A;Accession: JH0319

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-92 <BAI>

A;Cross-references: GB:X53682; NID:G34217; PIDN:CAA37723.1; PID:G34218

A;Experimental source: natural killer cell, strain CD3-CD2+, F5, SIIIE5

R;Napolitano, M.; Modi, W.S.; Cevario, S.J.; Gnarr, J.R.; Seuanez, H.N.; Leonard, W.J

Proc. Natl. Acad. Sci. U.S.A. 85, 9704-9708, 1988

A;Title: Identification, cloning, and characterization of an immune activation gene.

A;Reference number: A31767; MUID:89071764; PMID:2462251

A;Accession: A31767

A;Molecule type: mRNA

A;Residues: 1-92 <LIP>

A;Cross-references: GB:J04130; NID:G178017; PIDN:AAA51576.1; PID:G178018

R;Chang, H.C.; Reinherz, E.L.

Eur. J. Immunol. 19, 1045-1051, 1989

A;Title: Isolation and characterization of a cDNA encoding a putative cytokine which i

A;Reference number: A37411; MUID:89325421; PMID:2568930

A;Accession: A37411

A;Molecule type: mRNA

A;Residues: 1-92 <CHA>

A;Cross-references: GB:X16166; NID:G32035; PIDN:CAA34291.1; PID:G32036

R;Zipfel, P.F.; Balke, J.; Irving, S.G.; Kelly, K.; Siebenlist, U.

J. Immunol. 142, 1582-1590, 1989

A;Title: Mitogenic activation of human T cells induces two closely related genes which

A;Reference number: A30574; MUID:89140347; PMID:2521882

A;Accession: B30574

A;Molecule type: mRNA

A;Residues: 1-19, 'L', 21-92 <ZIP>

A;Cross-references: GB:M25316; NID:G602454; PIDN:AAA57256.1; PID:G602455

R;Miller, M.D.; Hata, S.; Malefyt, R.D.W.; Krangel, M.S.

ALIGNMENTS

Immunol. 143, 2907-2916, 1989  
 Title: A novel polypeptide secreted by activated human T lymphocytes.  
 Reference number: A45817; MUID:90038522; PMID:2809212  
 Accession: B45817  
 Molecule type: mRNA  
 Residues: 7-55, 'I', 57-79, 'T', 81-92 <MIL>  
 Cross-references: GB:M57503; NID:G3339726; PIDN:AAA36752.1; PID:G3339727  
 Brown, K.D.; Zurawski, S.M.; Mosmann, T.R.; Zurawski, G.  
 Immunol. 142, 679-687, 1989  
 Title: A family of small inducible proteins secreted by leukocytes are members of a new of various activation processes.  
 Reference number: A30552; MUID:89093958; PMID:2521353  
 Accession: D30552  
 Molecule type: mRNA  
 Residues: 1-39, 'REASS', 46-92 <BRO>  
 Cross-references: GB:M23502; NID:G533212; PIDN:AAA36656.1; PID:G533213  
 Clore, G.M.; Lodi, P.J.; Garrett, D.S.; Gronenborn, A.M.  
 Submitted to the Brookhaven Protein Data Bank, January 1994  
 Reference number: A52206; PDB:1HUM  
 Contents: annotation; conformation and disulfide bond assignments by (1)H-NMR, residue  
 Comment: This protein is secreted by activated lymphocytes and monocytes. It is bound  
 Genetics:  
 Gene: GDB:LAG1  
 Cross-references: GDB:127451; OMIM:153335  
 Map position: 17q21-17q21  
 Introns: 26/1; 64/2  
 Superfamily: macrophage inflammatory protein  
 Keywords: chemotaxis; cytokine; inflammation  
 1-23/Domain: signal sequence #status predicted <SIG>  
 24-92/Product: macrophage inflammatory protein 1-beta #status experimental <MAT>  
 34-58, 35-74/Disulfide bonds: #status experimental

Query Match 100.0%; Score 486; DB 1; Length 92;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-45;  
 Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 MKLCVTVLSLLMLVAAPCSAPMSDPTACCFSTARKLPNFFVVDYETSSLSQ 60  
 |||||  
 b 1 MKLCVTVLSLLMLVAAPCSAPMSDPTACCFSTARKLPNFFVVDYETSSLSQ 60  
 |||||

Y 61 PAVVFQTKRSKQVCADPSESQVQYVVDLELN 92  
 |||||  
 b 61 PAVVFQTKRSKQVCADPSESQVQYVVDLELN 92  
 |||||

RESULT 2  
 46730  
 Immune activation gene 2 - rabbit  
 Species: Oryctolagus cuniculus (domestic rabbit)  
 Date: 14-Feb-1997 #sequence\_revision 14-Feb-1997 #text\_change 16-Jul-1999  
 Accession: I46730  
 Mori, S.; Goto, K.; Goto, F.; Mutakami, K.; Ohkawara, S.; Yoshinaga, M.  
 Int. Immunol. 6, 149-156, 1994  
 Title: Dynamic changes in mRNA expression of neutrophils during the course of acute in  
 Reference number: I46730; MUID:94198229; PMID:8148323  
 Accession: I46730  
 Status: preliminary; translated from GB/EMBL/DDBJ  
 Molecule type: mRNA  
 Residues: 1-92 <MOR>  
 Cross-references: GB:D17402; NID:G599577; PIDN:BAA04226.1; PID:G599578  
 Superfamily: macrophage inflammatory protein

Query Match 84.2%; Score 409; DB 2; Length 92;  
 Best Local Similarity 82.6%; Pred. No. 4.6e-37;  
 Matches 76; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

2Y 1 MKLCVTVLSLLMLVAAPCSAPMSDPTACCFSTARKLPNFFVVDYETSSLSQ 60  
 |||||  
 Db 1 MKLCVTVLSVALLVAALCPPALSAAPMSDPTACCFSTARKLPNFFVVDYETSSLSQ 60  
 |||||

2Y 61 PAVVFQTKRSKQVCADPSESQVQYVVDLELN 92  
 |||||  
 Db 61 PAVVFQTKRSKQVCADPSESQVQYVVDLELN 92  
 |||||

RESULT 3  
 C30552  
 macrophage inflammatory protein 1-beta precursor - mouse  
 Alternate names: H400; SIS gamma; T-cell activation protein gamma  
 Species: Mus musculus (house mouse)  
 Date: 28-Aug-1989 #sequence\_revision 28-Aug-1989 #text\_change 16-Jul-1999  
 Accession: C30552; JLO088; PS0304; S22042  
 Brown, K.D.; Zurawski, S.M.; Mosmann, T.R.; Zurawski, G.  
 Immunol. 142, 679-687, 1989  
 Title: A family of small inducible proteins secreted by leukocytes are members of a new of various activation processes.  
 Reference number: A30552; MUID:89093958; PMID:2521353  
 Accession: C30552  
 Molecule type: mRNA  
 Residues: 1-92 <BRO>  
 Cross-references: GB:M23503; NID:G533244; PIDN:AAA40148.1; PID:G533245  
 Sherry, B.; Tekamp-Olson, P.; Gallegos, C.; Bauer, D.; Davatelis, G.; Wolpe, S.D.; M  
 J. Exp. Med. 168, 2251-2259, 1988  
 Title: Resolution of the two components of macrophage inflammatory protein 1, and cl  
 Reference number: JLO088; MUID:89067830; PMID:3058856  
 Accession: JLO088  
 Molecule type: mRNA  
 Residues: 1-92 <SHE>  
 Cross-references: GB:M35590; NID:G199696; PIDN:AAA39708.1; PID:G199697  
 Accession: PS0304  
 Molecule type: protein  
 Residues: 24-33, 'XX', 36, 'X', 38 <SH2>  
 Daubersies, P.; Lepretre, F.; Bailleul, B.; Grove, M.; Pragnell, I.; Plumb, M.  
 Submitted to the EMBL Data Library, October 1991  
 Description: Sequence of the murine macrophage inflammatory protein 1b gene.  
 Reference number: S22042  
 Accession: S22042  
 Status: preliminary  
 Molecule type: DNA  
 Residues: 1-92 <DAU>  
 Cross-references: EMBL:X62502; NID:G53126; PIDN:CAA44364.1; PID:G53127  
 Comment: This protein is a monokine.  
 Genetics:  
 Introns: 26/1; 64/2  
 Superfamily: macrophage inflammatory protein  
 Keywords: glycoprotein  
 1-23/Domain: signal sequence #status predicted <SIG>  
 24-92/Product: macrophage inflammatory protein 1-beta #status experimental <MAT>  
 76/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 80.2%; Score 390; DB 2; Length 92;  
 Best Local Similarity 76.1%; Pred. No. 5.1e-35;  
 Matches 70; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 MKLCVTVLSLLMLVAAPCSAPMSDPTACCFSTARKLPNFFVVDYETSSLSQ 60  
 |||||  
 Db 1 MKLCVSALLSLLVAAPCAPGFSAPMSDPTSCCFSTARKLPNFFVVDYETSSLSQ 60  
 |||||

QY 61 PAVVFQTKRSKQVCADPSESQVQYVVDLELN 92  
 |||||  
 Db 61 PAVVFQTKRSKQVCADPSESQVQYVVDLELN 92  
 |||||

RESULT 4  
 A32393  
 macrophage inflammatory protein-1-alpha precursor - mouse  
 Alternate names: heparin-binding chemotaxis protein; L2G25B protein; SCI/MIP-1a; SIS  
 Species: Mus musculus (house mouse)  
 Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 16-Jul-1999  
 Accession: S11685; A32393; S04533; A53885; A30552; PS0303; A27596; I56104  
 Grove, M.; Lowe, S.; Graham, G.; Pragnell, I.; Plumb, M.  
 Nucleic Acids Res. 18, 5561, 1990  
 Title: Sequence of the murine haemopoietic stem cell inhibitor/macrophage inflammato  
 Reference number: S11685; MUID:91016858; PMID:2216738  
 Accession: S11685  
 Molecule type: DNA

Residues: 1-92 <GRO>  
Cross-references: EMBL:X53372; NID:G54062; PIDN:CAA37452.1; PID:G297531  
Note: the authors' translation of the nucleotide sequence differs at several positions  
Kwon, B.S.; Weissman, S.M.  
DC. Natl. Acad. Sci. U.S.A. 86, 1963-1967, 1989  
Title: cDNA sequence of two inducible T-cell genes.  
Reference number: A32393; MUID:89184547; PMID:2784565  
Accession: A32393  
Molecule type: mRNA  
Residues: 1-92 <KWO>  
Cross-references: GB:J04491; NID:G201524; PIDN:AAA40304.1; PID:G201525  
Davatelis, G.; Tekamp-Olson, P.; Wolpe, S.D.; Hermesen, K.; Luedke, C.; Gallegos, C.;  
Exp. Med. 167, 1939-1944, 1988  
Title: Cloning and characterization of a cDNA for murine macrophage inflammatory prote  
Reference number: S04533; MUID:88258380; PMID:3290382  
Accession: S04533  
Molecule type: mRNA  
Residues: 1-48, 'E', '50-90, 'I', '92 <DA2>  
Cross-references: EMBL:X12531  
Note: the authors translated the codon GAG for residue 49 as Asp and ATT for residue 9  
Note: the sequence has been corrected in reference A53885  
Davatelis, G.; Tekamp-Olson, P.; Wolpe, S.D.; Hermesen, K.; Luedke, C.; Gallegos, C.;  
Exp. Med. 170, 2189, 1989  
Reference number: A53885  
Contents: erratum  
Accession: A53885  
Molecule type: mRNA  
Residues: 1-92 <DAV>  
Cross-references: EMBL:X12531; NID:G53122; PIDN:CAA31047.1; PID:G53123  
Brown, K.D.; Zurawski, S.M.; Mosmann, T.R.; Zurawski, G.  
Immunol. 142, 679-687, 1989  
Title: A family of small inducible proteins secreted by leukocytes are members of a ne  
of various activation processes.  
Reference number: A30552; MUID:89093958; PMID:2521353  
Accession: A30552  
Molecule type: mRNA  
Residues: 1-21, 'L', '23-61, 'A', '63-92 <BRO>  
Cross-references: GB:M23447; NID:G533240; PIDN:AAA40146.1; PID:G533241  
Sherry, B.; Tekamp-Olson, P.; Gallegos, C.; Bauer, D.; Davatelis, G.; Wolpe, S.D.; Mas  
Exp. Med. 168, 2251-2259, 1988  
Title: Resolution of the two components of macrophage inflammatory protein 1, and clon  
Reference number: JLO088; MUID:89067830; PMID:3058856  
Accession: PS0303  
Molecule type: mRNA  
Residues: 24-33, 'XX', '36-54 <SHE>  
Wolpe, S.D.; Davatelis, G.; Sherry, B.; Beutler, B.; Hesse, D.G.; Nguyen, H.T.; Moldaw  
Exp. Med. 167, 570-581, 1988  
Title: Macrophages secrete a novel heparin-binding protein with inflammatory and neut  
Reference number: A27596; MUID:88154745; PMID:3279154  
Accession: A27596  
Molecule type: protein  
Residues: 24-33, 'XX', '36-42 <WOL>  
Note: 26-Met, 30-Pro, and 39-Thr were also found  
Widmer, U.; Yang, Z.; van Deventer, S.; Manogue, K.R.; Sherry, B.; Cerami, A.  
Immunol. 146, 4031-4040, 1991  
Title: Genomic structure of murine macrophage inflammatory protein-1-alpha and conserv  
Reference number: I56104; MUID:91237116; PMID:2033269  
Accession: I56104  
Status: preliminary; translated from GB/EMBL/DBJ  
Molecule type: DNA  
Residues: 1-92 <RES>  
Cross-references: GB:M73061; NID:G199694; PIDN:AAA39707.1; PID:G199695  
Comment: This protein is a monokine.  
Genetics:  
Introns: 23/3; 26/1; 63/2  
Superfamily: macrophage inflammatory protein  
Keywords: heparin binding  
1-23/Domain: signal sequence #status predicted <SIG>  
24-92/Product: macrophage inflammatory protein #status experimental <MAT>  
Query Match 65.9%; Score 320.5; DB 2; Length 92;  
Best Local Similarity 60.9%; Pred. No. 1.6e-27;  
Matches 56; Conservative 16; Mismatches 19; Indels 1; Gaps 1;

QY 1 MKLCVTVLSLLMLVAAFCSPALSGDPPTACCFSTYARKLPNRFVVDYETSSLSQ 60  
Db 1 MKVSTTALAVLLCTMTLCNQVSPAPYGADTPTACCFSTY-SRKIPRQFIVDYFETSSLSQ 59  
QY 61 PAVVFQTKRSKQVCADPSESWQVQYVYDLELN 92  
Db 60 PGVIFLTGRQVCAADPSKQVQYVYDLELN 91  
RESULT 5  
B35673  
LD78-beta protein precursor - human  
N/Alternate names: macrophage inflammatory protein homolog GOS19-2; small inducible cy  
C/Species: Homo sapiens (man)  
C/Date: 28-Sep-1990 #sequence\_revision 28-Sep-1990 #text\_change 20-Jun-2000  
C/Accession: B35673; B30412; S10157; B30908  
R/Nakao, M.; Nomiyama, H.; Shimada, K.  
Mol. Cell. Biol. 10, 3646-3658, 1990  
A/Title: Structures of human genes coding for cytokine LD78 and their expression.  
A/Reference number: A35673; MUID:90287155; PMID:1694014  
A/Accession: B35673  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-93 <NAK>  
A/Cross-references: GB:D90145; NID:G219907; PIDN:BAA14173.1; PID:G219908  
R/Blum, S.; Forsdyke, R.E.; Forsdyke, D.R.  
DNA Cell Biol. 9, 589-602, 1990  
A/Title: Three human homologs of a murine gene encoding an inhibitor of stem cell prol  
A/Reference number: A30412; MUID:91103879; PMID:2271120  
A/Accession: B30412  
A/Status: preliminary; not compared with conceptual translation  
A/Molecule type: DNA  
A/Residues: 1-93 <BLU>  
A/Cross-references: GB:M24110; GB:M32338; NID:G182848; PIDN:AAA35859.1; PID:G182849  
R/Irving, S.G.; Zipfel, P.F.; Balke, J.; McBride, O.W.; Morton, C.C.; Burd, P.R.; Sieb  
Nucleic Acids Res. 18, 3261-3270, 1990  
A/Title: Two inflammatory mediator cytokine genes are closely linked and variably ampli  
A/Reference number: S10157; MUID:90287702; PMID:1972563  
A/Accession: S10157  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-93 <IRV>  
A/Cross-references: EMBL:X52149; NID:G34750; PIDN:CAA36397.1; PID:G296666  
C/Comment: This protein is a member of a "small inducible" or "activation specific" ge  
C/Genetics:  
A/Gene: GDB:SCYA4  
A/Cross-references: GDB:120369; OMIM:182284  
A/Map position: 17q11-17q21  
A/Introns: 26/1; 64/2  
C/Superfamily: macrophage inflammatory protein  
C/Keywords: cytokine  
F/1-22/Domain: signal sequence #status predicted <SIG>  
F/23-93/Product: LD78-beta protein #status predicted <MAT>  
Query Match 65.8%; Score 320; DB 2; Length 93;  
Best Local Similarity 58.7%; Pred. No. 1.8e-27;  
Matches 54; Conservative 20; Mismatches 18; Indels 0; Gaps 0;  
QY 1 MKLCVTVLSLLMLVAAFCSPALSGDPPTACCFSTYARKLPNRFVVDYETSSLSQ 60  
Db 1 MQVSTAALAVLLCTMTLCNQVLSAPLAADTPTACCFSTYRSQIPQNFIAFYETSSQCSK 60  
QY 61 PAVVFQTKRSKQVCADPSESWQVQYVYDLELN 92  
Db 61 PSVIFLTGRQVCAADPSSEWQVQYVYDLELN 92  
RESULT 6  
I52322  
macrophage inflammatory protein-1alpha - rat  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 16-Jul-1999



```
F;33-57,34-73/Disulfide bonds: #status predicted
```

Query Match 61.8%; Score 300.5; DB 2; Length 92;  
Best Local Similarity 57.6%; Pred. No. 2.3e-25;  
Matches 53; Conservative 19; Mismatches 19; Indels 1; Gaps 1;

OY 1 MKLCVTVLSLLMLVAACFSPALSPMGSDPPTACCFSYTARKLPNFVVDDYETSSLSQ 60  
|::||::||::||::||::||::||::||::||::||::||::||::||::||::||  
DB 1 MQVSTAALAVLLCTMALCN-QFSASLAADTPTACCFSYTSRQPONFIADYFETSSQCSK 59  
|::||::||::||::||::||::||::||::||::||::||::||::||::||::||  
OY 61 PAVVFQTKRSKQVCADPPSESWVQEYVVDLELN 92  
|::||::||::||::||::||::||::||::||::||::||::||::||::||::||  
DB 60 PGVIFLTKRNRQICADPKETWVQEYITELELN 91  
|::||::||::||::||::||::||::||::||::||::||::||::||::||::||

RESULT 8  
C60407  
monocyte adherence-induced protein 5 beta - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 06-Nov-1992 #sequence\_revision 06-Nov-1992 #text\_change 03-May-1996  
C;Accession: C60407  
R;Sporn, S.A.; Eierman, D.F.; Johnson, C.E.; Morris, J.; Martin, G.; Ladner, M.; Haski  
J. Immunol. 144, 4434-4441, 1990  
A;Title: Monocyte adherence results in selective induction of novel genes sharing hom  
A;Reference number: A60407; MUID:90257367; PMID:2341726  
A;Accession: C60407  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-50 <SPO>  
C;Superfamily: macrophage inflammatory protein

Query Match 54.1%; Score 263; DB 2; Length 50;  
Best Local Similarity 98.0%; Pred. No. 1.4e-21;  
Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 43 LPRNFFVDDYETSSLSQSPAVVFTKRSKQVCADPPSESWVQEYVVDLELN 92  
:||||||||||||||||||||||||||||||||||||||||||||||||||  
DB 1 VPRNFFVDDYETSSLSQSPAVVFTKRSKQVCADPPSESWVQEYVVDLELN 50  
:||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 9  
A28815  
monocyte chemoattractant cytokine RANTES precursor - human  
N;Alternate names: small inducible cytokine A5; T-cell specific cytokine RANTES  
C;Species: Homo sapiens (man)  
C;Date: 30-Jun-1989 #sequence\_revision 16-Aug-1996 #text\_change 29-May-1998  
C;Accession: A28815  
R;Schall, T.J.; Jongstra, J.; Dyer, B.J.; Jorgensen, J.; Clayberger, C.; Davis, M.M.;  
J. Immunol. 141, 1018-1025, 1988  
A;Title: A human T cell-specific molecule is a member of a new gene family.  
A;Reference number: A28815; MUID:88285659; PMID:2456327  
A;Accession: A28815  
A;Molecule type: mRNA  
A;Residues: 1-91 <SCH>  
A;Cross-references: GB:M21121  
C;Comment: The acronym RANTES reflects the description "Regulated upon Activation, No  
C;Genetics:  
A;Gene: GDB:SCYA5; D17S136E  
A;Cross-references: GDB:I20749; OMIM:187011  
A;Map position: 17q11.2-17q12  
C;Superfamily: macrophage inflammatory protein  
C;Keywords: chemotaxis; cytokine; immediate-early protein; inflammation; T-cell  
F;1-23/Domain: signal sequence #status predicted <SIG>  
F;24-91/Product: T-cell protein RANTES #status predicted <MAT>

Query Match 50.5%; Score 245.5; DB 1; Length 91;  
Best Local Similarity 45.7%; Pred. No. 1.9e-19;  
Matches 42; Conservative 23; Mismatches 26; Indels 1; Gaps 1;

OY 1 MKLCVTVLSLLMLVAACFSPALSPMGSDPPTACCFSYTARKLPNFVVDDYETSSLSQ 60  
|::||::||::||::||::||::||::||::||::||::||::||::||::||::||  
DB 1 MKVSAAALAVILIATLALCAPASAPSYSSD-TTPCCPAYIARPLPRAHKEYFYFTSGKCSN 59  
|::||::||::||::||::||::||::||::||::||::||::||::||::||::||

Accession: I52322  
Shi, M.M.; Godleski, J.J.; Paulauskis, J.D.  
ochem. Biophys. Res. Commun. 211, 289-295, 1995  
Title: Molecular cloning and posttranscriptional regulation of macrophage inflammatory  
Reference number: I52322; MUID:95298037; PMID:7779098  
Accession: I52322  
Status: preliminary; translated from GB/EMBL/DDBJ  
Molecule type: mRNA  
Residues: 1-92 <RES>  
Cross-references: EMBL:U22414; NID:g790632; PIDN:AAA80608.1; PID:g790633  
Superfamily: macrophage inflammatory protein

Query Match 62.4%; Score 303.5; DB 2; Length 92;  
Best Local Similarity 57.6%; Pred. No. 1.1e-25;  
Matches 53; Conservative 17; Mismatches 21; Indels 1; Gaps 1;

1 MKLCVTVLSLLMLVAACFSPALSPMGSDPPTACCFSYTARKLPNFVVDDYETSSLSQ 60  
|::||::||::||::||::||::||::||::||::||::||::||::||::||::||  
1 MKVSTAALAVLLCTMALNWNEVFSAPYGADTPTACCFSY-GRQIPRKFIADYFETSSLSQ 59  
|::||::||::||::||::||::||::||::||::||::||::||::||::||::||  
61 PAVVFQTKRSKQVCADPPSESWVQEYVVDLELN 92  
|::||::||::||::||::||::||::||::||::||::||::||::||::||::||  
60 PGVIFLTKRNRQICADPKETWVQEYITELELN 91  
|::||::||::||::||::||::||::||::||::||::||::||::||::||::||

RESULT 7  
I0574  
macrophage inflammatory protein 1-alpha precursor - human  
Alternate names: LD78-alpha protein precursor; lymphocyte tumor promoter-induced prote  
ination protein 1  
Species: Homo sapiens (man)  
Date: 03-Aug-1992 #sequence\_revision 03-Aug-1992 #text\_change 21-Jul-2000  
Accession: A35673; A30574; A30412; A24198; A30908  
Nakao, M.; Nomiya, H.; Shimada, K.  
l. Cell. Biol. 10, 3646-3658, 1990  
Title: Structures of human genes coding for cytokine LD78 and their expression.  
Reference number: A35673; MUID:90287155; PMID:1694014  
Accession: A35673  
Molecule type: DNA  
Residues: 1-92 <NAK>  
Cross-references: GB:D90144; NID:g219905; PIDN:BAA14172.1; PID:g219906  
Zipfel, P.F.; Balke, J.; Irving, S.G.; Kelly, K.; Siebenlist, U.  
Immunol. 142, 1582-1590, 1989  
Title: Mitogenic activation of human T cells induces two closely related genes which e  
Reference number: A30574; MUID:89140347; PMID:2521882  
Accession: A30574  
Molecule type: mRNA  
Residues: 1-92 <ZIP>  
Cross-references: GB:M25315; NID:g602452; PIDN:AAA57255.1; PID:g602453  
Blum, S.; Forsdyke, R.E.; Forsdyke, D.R.  
NA Cell Biol. 9, 589-602, 1990  
Title: Three human homologs of a murine gene encoding an inhibitor of stem cell prolif  
Reference number: A30412; MUID:91103879; PMID:2271120  
Accession: A30412  
Molecule type: mRNA  
Residues: 1-92 <BUJ>  
Cross-references: GB:M23178; GB:M32337; NID:g182846; PIDN:AAA35858.1; PID:g182847  
Obaru, K.; Fukuda, M.; Maeda, S.; Shimada, K.  
Biochem. 99, 885-894, 1986  
Title: A cDNA clone used to study mRNA inducible in human tonsillar lymphocytes by a b  
Reference number: A24198; MUID:86223879; PMID:3086300  
Accession: A24198  
Status: preliminary  
Molecule type: mRNA  
Residues: 1-92 <OBA>  
Cross-references: GB:X03754; NID:g34298; PIDN:CAA27388.1; PID:g758089  
Genetics:  
Gene: GDB:SCYA3  
Cross-references: GDB:I20368; OMIM:182283  
Map position: 17q11-17q21  
Superfamily: macrophage inflammatory protein  
1-20/Domain: signal sequence #status predicted <SIG>  
21-92/Product: macrophage inflammatory protein 1-alpha #status predicted <MAT>

```
F;33-57,34-73/Disulfide bonds: #status predicted
```

Query Match 61.8%; Score 300.5; DB 2; Length 92;  
Best Local Similarity 57.6%; Pred. No. 2.3e-25;  
Matches 53; Conservative 19; Mismatches 19; Indels 1; Gaps 1;

QY 1 MKLCVTVLSLLMLVAAFCSPPALSAPMGSDPPTACCFSTARKLPNFVVDDYETSSLSQS 60  
|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||  
Db 1 MQVSTAALAVLLCTMALCN-QFSASLAADTPTACCFSTSRQPONFIADYFETSSQCSK 59  
|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||

QY 61 PAVVFQTKRSKQVCADPSESWSWQEVVVDLELN 92  
|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||  
Db 60 PGVIFLTKRNRQICADPKETWVQVEYTELELN 91  
|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||

RESULT 8  
C60407  
monocyte adherence-induced protein 5 beta - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 06-Nov-1992 #sequence\_revision 06-Nov-1992 #text\_change 03-May-1996  
C;Accession: C60407  
R;Sporn, S.A.; Eierman, D.F.; Johnson, C.E.; Morris, J.; Martin, G.; Ladner, M.; Haski  
J. Immunol. 144, 4434-4441, 1990  
A;Title: Monocyte adherence results in selective induction of novel genes sharing hom  
A;Reference number: A60407; MUID:90257367; PMID:2341726  
A;Accession: C60407  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-50 <SPO>  
C;Superfamily: macrophage inflammatory protein

Query Match 54.1%; Score 263; DB 2; Length 50;  
Best Local Similarity 98.0%; Pred. No. 1.4e-21;  
Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 43 LPRNFFVDDYETSSLSQSQAFAVVFQTKRSKQVCADPSESWSWQEVVVDLELN 92  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 1 VPRNFFVDDYETSSLSQSQAFAVVFQTKRSKQVCADPSESWSWQEVVVDLELN 50  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 9  
A28815  
monocyte chemoattractant cytokine RANTES precursor - human  
N;Alternate names: small inducible cytokine A5; T-cell specific cytokine RANTES  
C;Species: Homo sapiens (man)  
C;Date: 30-Jun-1989 #sequence\_revision 16-Aug-1996 #text\_change 29-May-1998  
C;Accession: A28815  
R;Schall, T.J.; Jongstra, J.; Dyer, B.J.; Jorgensen, J.; Clayberger, C.; Davis, M.M.;  
J. Immunol. 141, 1018-1025, 1988  
A;Title: A human T cell-specific molecule is a member of a new gene family.  
A;Reference number: A28815; MUID:88285659; PMID:2456327  
A;Accession: A28815  
A;Molecule type: mRNA  
A;Residues: 1-91 <SCH>  
A;Cross-references: GB:M21121  
C;Comment: The acronym RANTES reflects the description "Regulated upon Activation, No  
C;Genetics:  
A;Gene: GDB:SCYA5; D17S136E  
A;Cross-references: GDB:I20749; OMIM:187011  
A;Map position: 17q11.2-17q12  
C;Superfamily: macrophage inflammatory protein  
C;Keywords: chemotaxis; cytokine; immediate-early protein; inflammation; T-cell  
F;1-23/Domain: signal sequence #status predicted <SIG>  
F;24-91/Product: T-cell protein RANTES #status predicted <MAT>

Query Match 50.5%; Score 245.5; DB 1; Length 91;  
Best Local Similarity 45.7%; Pred. No. 1.9e-19;  
Matches 42; Conservative 23; Mismatches 26; Indels 1; Gaps 1;

QY 1 MKLCVTVLSLLMLVAAFCSPPALSAPMGSDPPTACCFSTARKLPNFVVDDYETSSLSQS 60  
|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||  
Db 1 MKVSAAALAVILIATLALCAPASASPYSST-TTPCCFAYIARPLPRAHKEYFYFTSGKCSN 59  
|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||

SULT 10  
6539  
nocyte chemoattractant cytokine RANTES precursor - mouse  
Alternate names: MuRantes  
Species: Mus musculus (house mouse)  
Date: 18-Jun-1993 #sequence revision 16-Aug-1996 #text\_change 22-Jun-1999  
Accession: I48875; A46539; I48554; I56970  
Danoff, T.M.; Lalley, P.A.; Chang, Y.S.; Heeger, P.S.; Neilson, E.G.  
Immunol. 152, 1182-1189, 1994  
Title: Cloning, genomic organization, and chromosomal localization of the Scya5 gene  
Reference number: I48875; MUID:94132613; PMID:7507961  
Accession: I48875  
Status: preliminary; translated from GB/EMBL/DBJ  
Molecule type: DNA  
Residues: 1-91 <DAN>  
Cross-references: EMBL:U02298; NID:G460090; PIDN:AAA18302.1; PID:G460091  
Schall, T.J.; Simpson, N.J.; Mak, J.Y.  
r. J. Immunol. 22, 1477-1481, 1992  
Title: Molecular cloning and expression of the murine RANTES cytokine: structural and  
Reference number: A46539; MUID:92289805; PMID:1376260  
Accession: A46539  
Molecule type: mRNA  
Residues: 1-18, 'A', 20-91 <SCH>  
Cross-references: GB:S37648; NID:G250207; PIDN:AAB22330.1; PID:G250208  
Experimental source: macrophage cell line PU5-1.8  
Note: sequence extracted from NCBI backbone (NCBIN:106768, NCBIP:106770)  
Shin, H.S.; Drysdale, B.E.; Shin, M.L.; Noble, P.W.; Fisher, S.N.; Paznekas, W.A.  
1. Cell. Biol. 14, 2914-2925, 1994  
Title: Definition of a lipopolysaccharide-responsive element in the 5'-flanking region  
Reference number: I48654; MUID:94217689; PMID:7513046  
Accession: I48654  
Status: translation not shown; translated from GB/EMBL/DBJ  
Molecule type: DNA  
Residues: 1-91 <SHI>  
Cross-references: EMBL:X70675; NID:G475205; PIDN:CAA50011.1; PID:G475206  
Neilson, E.G.; Krensky, A.  
dney Int. 41, 220-225, 1992  
Title: Isolation and characterization of cDNA from renal tubular epithelium encoding m  
Reference number: I56970; MUID:92277990; PMID:1375672  
Accession: I56970  
Status: translated from GB/EMBL/DBJ  
Molecule type: mRNA  
Residues: 1-40, 'E', 42-91 <NEI>  
Cross-references: GB:M77747; NID:G200649; PIDN:AAA40029.1; PID:G200650  
Comment: This chemoattractant for monocytes but not neutrophils is an immediate-early  
Genetics:  
Introns: 26/1; 63/2  
Superfamily: macrophage inflammatory protein  
Keywords: chemotaxis; cytokine; immediate-early protein; inflammation  
1-23/Domain: signal sequence #status predicted <SIG>  
24-91/Product: monocyte chemoattractant cytokine RANTES #status predicted <MAT>  
Query Match 49.9%; Score 242.5; DB 1; Length 91;  
Best Local Similarity 48.9%; Pred. No. 4e-19;  
Matches 45; Conservative 20; Mismatches 26; Indels 1; Gaps 1;  
1 MKLCVTVLSLLMLVAAFCSPPALSGSDPPTACCFSTYARKLPNFVVDYVETSSLCQ 60  
1 MKISAAALTILTAALACTPAPASPYGSD-TTPCCFAYLSLALPRAHVKEYFYTSSKCSN 59  
61 PAVVFQTKRSKQVCADPSESWSVQYVVDLELN 92  
60 LAVVFVTRNRQVCANPEKKWQYVINYLEMS 91

SULT 11

17723

mediate-early serum-responsive protein JE precursor - rat

N;Alternate names: monocyte chemoattractant protein-1  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text\_change 10-Sep-1999  
C;Accession: S07723; JN0128  
R;Timmers, H.T.M.; Pronk, G.J.; Bos, J.L.; van der Eb, A.J.  
Nucleic Acids Res. 18, 23-34, 1990  
A;Title: Analysis of the rat JE gene promoter identifies an AP-1 binding site essential  
A;Reference number: S07723; MUID:90174947; PMID:2106664  
A;Accession: S07723  
A;Molecule type: DNA  
A;Residues: 1-148 <TIM>  
A;Cross-references: EMBL:X17053; NID:G55530; PIDN:CAA34901.1; PID:G55531  
R;Yoshimura, T.; Takeya, M.; Takahashi, K.  
Biochem. Biophys. Res. Commun. 174, 504-509, 1991  
A;Title: Molecular cloning of rat monocyte chemoattractant protein-1 (MCP-1) and its  
A;Reference number: JN0128; MUID:91128376; PMID:1704226  
A;Accession: JN0128  
A;Molecule type: mRNA  
A;Residues: 1-148 <YOS>  
A;Cross-references: GB:M57441; NID:G205333; PIDN:AAA63496.1; PID:G205334  
A;Experimental source: spleen cells  
A;Note: the authors translated the codon GAA for residue 62 as Lys and GCT for residue  
C;Genetics:  
A;Introns: 26/1; 65/2  
C;Superfamily: macrophage inflammatory protein  
F;1-23/Domain: signal sequence #status predicted <SIG>  
F;24-148/Product: immediate-early serum-responsive protein JE #status predicted <MAT>  
Query Match 40.6%; Score 197.5; DB 1; Length 148;  
Best Local Similarity 41.9%; Pred. No. 4.6e-14;  
Matches 39; Conservative 20; Mismatches 33; Indels 1; Gaps 1;  
QY 1 MKLCVTVLSLLMLVAAFCSPPALSGSDPPTACCFSTYARKLPNFVVDYVETSSLCQ 59  
Db 1 MQVSVTLGLFTVAACSIHVLSQPDVAVNAPLTCCYSFTGKMPMSRLNRYKRTSSRCP 60  
QY 60 QPAVVFQTKRSKQVCADPSESWSVQYVVDLELN 92  
Db 61 KEAVVFVTKLREICADPNKEWQYKIRKLDQN 93  
RESULT 12  
A54678  
monocyte chemotactic protein 3 precursor - human  
N;Alternate names: monocyte chemoattractant protein MCP-3  
C;Species: Homo sapiens (man)  
C;Date: 28-Oct-1994 #sequence revision 28-Oct-1994 #text\_change 16-Jul-1999  
C;Accession: A54678; JCI478; S32222  
R;Opdenakker, G.; Fiten, P.; Nys, G.; Froyen, G.; Van Roy, N.; Speleman, F.; Laureys, G.  
Genomics 21, 403-408, 1994  
A;Title: The human MCP-3 gene (SCYA7): cloning, sequence analysis, and assignment to  
A;Reference number: A54678; MUID:94375065; PMID:7916328  
A;Accession: A54678  
A;Molecule type: DNA  
A;Residues: 1-109 <OPD>  
A;Cross-references: GB:X72309  
R;Opdenakker, G.; Froyen, G.; Fiten, P.; Proost, P.; Van Damme, J.  
Biochem. Biophys. Res. Commun. 191, 535-542, 1993  
A;Title: Human monocyte chemotactic protein-3 (MCP-3): Molecular cloning of the cDNA a  
A;Reference number: JCI478; MUID:93213290; PMID:8461011  
A;Accession: JCI478  
A;Molecule type: mRNA  
A;Residues: 1-109 <OP2>  
A;Cross-references: GB:X72308; GB:S57464; NID:G3928270; PIDN:CAA51055.1; PID:G313708  
R;Minty, A.; Chalon, P.; Guillemot, J.C.; Kaghad, M.; Liauzun, P.; Magazin, M.; Miloux  
submitted to the EMBL Data Library, March 1993  
A;Description: Molecular cloning of MCP-3: a human monocyte-derived monocyte chemoattr  
A;Reference number: S32222  
A;Accession: S32222  
A;Molecule type: mRNA  
A;Residues: 1-109 <MIN>  
A;Cross-references: EMBL:X71087; NID:G288396; PIDN:CAA50405.1; PID:G288397  
C;Comment: This protein induces proteinase secretion and chemotaxis by macrophages and

```
J. Immunol. 150, 5025-5032, 1993
A;Title: cDNA cloning of guinea pig monocyte chemoattractant protein-1 and expression
A;Reference number: I48147; MUID:93267104; PMID:8496603
A;Accession: I48147
A;Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A;Residues: 1-120 <RES>
A;Cross-references: GB:L04985; NID:g349820; PIDN:AAA37047.1; PID:g349821
C;Genetics:
A;Gene: MCP-1
C;Superfamily: macrophage inflammatory protein

Query Match      37.8%; Score 183.5; DB 2; Length 120;
Best Local Similarity 40.7%; Pred.No. 1.2e-12;
Matches 37; Conservative 23; Mismatches 28; Indels 3; Gaps 3;

QY      1 MKLCVTVLSLLMLVAFCSPALSAAPMGSDPPTACCFSTARKLPNRFVVDDYE-TSSLCS 59
       : |||:: |||| :: |:: |||:: |||:: |||:: |||:: |||:: |||:: |||
Db      1 MQRSSVLLCLLVTEATFCSLLMAQPDGVNTPT-CCYTFN-KQIPLKRVKGYERITSSRCP 58
       : |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||

QY      60 QPAVVFQTKRSKQVCADPSESWSVQEYVVDLE 90
       |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||
Db      59 QEAVIFRTLKNKEVCADPTQKWVDYIAKL D 89
       |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||

RESULT 15
JC2136
monocyte chemoattractant protein-1 precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 16-Jul-1999
C;Accession: JC2136; S57498
R;Hosang, K.; Knoke, I.; Klaudiny, J.; Wempe, F.; Wuttke, W.; Scheit, K.H.
Biochem. Biophys. Res. Commun. 199, 962-968, 1994
A;Title: Porcine luteal cells express monocyte chemoattractant protein-1 (MCP-1): Ana
A;Reference number: JC2136; MUID:94183284; PMID:7510962
A;Accession: JC2136
A:Molecule type: mRNA
A;Residues: 1-99 <HOS>
A;Cross-references: GB:Z48479; NID:g683716; PIDN:CAA88370.1; PID:g683717
R;Zach, O.
submitted to the EMBL Data Library, July 1994
A;Reference number: S57497
A;Accession: S57498
A;Status: preliminary
A:Molecule type: mRNA
A;Residues: 1-99 <ZAC>
A;Cross-references: EMBL:X79416; NID:g872312; PIDN:CAA55945.1; PID:g872313
C;Superfamily: macrophage inflammatory protein
C;Keywords: glycoprotein
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-99/Product: monocyte chemoattractant protein-1 #status predicted <MAT>
F;94/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match      37.1%; Score 180.5; DB 2; Length 99;
Best Local Similarity 35.2%; Pred. No. 2.1e-12;
Matches 32; Conservative 23; Mismatches 35; Indels 1; Gaps 1;

QY      1 MKLCVTVLSLLMLVAFCSPALSAAPMGSDPPTACCFSTARKLPNRFVVDDYE-TSSLCS 59
       |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||
Db      1 MKVSAALLCLLTAAFTCTQVLAQPDAINSPVTCCTTLTSKKISMQLMSYRRVTSSKCP 60
       |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||

QY      60 QPAVVFQTKRSKQVCADPSESWSVQEYVVDLE 90
       : |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||
Db      61 KEAVIFKTIAGKEICAEPKQKWQDSISHL D 91
       : |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||:: |||

Search completed: December 16, 2003, 15:40:57
Job time : 14:5738 secs
```

```

Genetics:
Gene: GDB:SCYA7; SCYA6; MCP-3
Cross-references: GDB:138473; OMIM:158106
Map position: 17q11-17q12
Introns: 36/1; 75/2
Superfamily: macrophage inflammatory protein
Keywords: cytokine; glycoprotein; inflammation
1-33/Domain: signal sequence #status predicted <SIG>
34-109/Product: monocyte chemotactic protein 3 #status predicted <MAT>
39/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match          39.6%; Score 192.5; DB 2; Length 109;
Best Local Similarity 38.5%; Pred. No. 1.2e-13;
Matches 35; Conservative 22; Mismatches 33; Indels 1; Gaps 1;

      1 MKLCVTVLSLLMLVAAFCSPALSAAPMGSDPPTACCFSYTARKLPNFWVDYYE-TSSLCS 59
      |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
11 MKASAALLCLLLTAAAFSPQGLAQPVGINTSTTCCYRFINKKIPKORLESYRRTTSSHP 70
      |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
      60 QPAVVVFQTKRSKQVCADPSESWSVQEVYVDLE 90
      :||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
71 REAVIFTKTKLDEICADPTQKWVQDFMKHLD 101
      |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

;RESULT 13
;0209
;GF-inducible JE glycoprotein precursor - mouse
;Species: Mus musculus (house mouse)
;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 10-Sep-1999
;Accession: A30209; A44771; A30861
;Rollins, B.J.; Morrison, E.D.; Stiles, C.D.
oc. Natl. Acad. Sci. U.S.A. 85, 3738-3742, 1988
;Title: Cloning and expression of JE, a gene inducible by platelet-derived growth factor
;Reference number: A30209; MUID:88234501; PMID:3287374
;Accession: A30209
;Molecule type: DNA
;Residues: 1-148 <ROL>
;Cross-references: GB:M19681; NID:G193486; PIDN:AAA37684.1; PID:G387168; GB:M19682
;Kawahara, R.S.; Deuel, T.F.
. Biol. Chem. 264, 679-682, 1989
;Title: Platelet-derived growth factor-inducible gene JE is a member of a family of sma
;Reference number: A44771; MUID:89093129; PMID:2910858
;Accession: A44771
;Molecule type: DNA; mRNA
;Residues: 1-148 <KA2>
;Cross-references: GB:J04467; NID:G193488; PIDN:AAA37685.1; PID:G387169
;Genetics:
;Gene: JE
;Introns: 26/1; 65/2
;Superfamily: macrophage inflammatory protein
;Keywords: cytokine; glycoprotein
;126/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match          38.2%; Score 185.5; DB 1; Length 148;
Best Local Similarity 39.8%; Pred. No. 9e-13;
Matches 37; Conservative 20; Mismatches 35; Indels 1; Gaps 1;

      1 MKLCVTVLSLLMLVAAFCSPALSAAPMGSDPPTACCFSYTARKLPNFWVDYYE-TSSLCS 59
      |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
      1 MQVPVMLLGLLFTVAGWSIHVLAQPDVAVNAPLTCYSFSTSKMIPMSRLESYKRITSSRCP 60
      |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
      60 QPAVVVFQTKRSKQVCADPSESWSVQEVYVDLELN 92
      :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
      61 KEAVVFVTKLKEVFCADPKKEWVQTYTKNLDNRN 93
      |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

;RESULT 14
;48147
monocyte chemoattractant protein-1 - guinea pig
;Species: Cavia porcellus (guinea pig)
;Date: 02-Jul-1996 #sequence revision 02-Jul-1996 #text_change 16-Jul-1999
;Accession: I48147
;Yoshimura, T.

```

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

protein - protein search, using sw model

non: December 16, 2003, 15:36:20 ; Search time 10.5574 Seconds  
(without alignments)  
409.804 Million cell updates/sec

tle: US-09-920-137A-7  
rfect score: 486  
quence: 1 MKLCVTVLSLLMLVAFCSP.....VCADPSESWWQEVYVDLELN 92

oring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

arched: 127863 seqs, 47026705 residues 127863  
tal number of hits satisfying chosen parameters:

nimum DB seq length: 0  
ximum DB seq length: 2000000000

st-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

tabase : SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	486	100.0	92	1 SY04_HUMAN	P13236 h small ind
2	409	84.2	92	1 SY04_RABIT	P46632 oryctolagus
3	394	81.1	92	1 SY04_RAT	P50230 rattus norv
4	390	80.2	92	1 SY04_MOUSE	P14097 mus musculu
5	320.5	65.9	92	1 SY03_MOUSE	P10855 mus musculu
6	320	65.8	93	1 SY3L_HUMAN	P16619 homo sapien
7	303.5	62.4	92	1 SY03_RAT	P50229 rattus norv
8	300.5	61.8	92	1 SY03_HUMAN	P10147 homo sapien
9	264	54.3	90	1 SY04_CHICK	Q90826 gallus gall
10	246.5	50.7	91	1 SY05_BOVIN	Q97919 bos taurus
11	245.5	50.5	91	1 SY05_HUMAN	P13501 homo sapien
12	242.5	49.9	91	1 SY05_MOUSE	P30882 mus musculu
13	238.5	49.1	91	1 SY05_SIGHI	Q91211 sigmodon hi
14	234.5	48.3	91	1 SY05_CAVPO	P97272 cavia porce
15	229	47.1	92	1 SY05_RAT	P50231 rattus norv
16	224.5	46.2	93	1 SY14_HUMAN	Q16627 homo sapien
17	210	43.2	89	1 SY18_HUMAN	P55774 h small ind
18	199	40.9	98	1 SY13_HUMAN	Q99616 homo sapien
19	197.5	40.6	148	1 SY02_RAT	P14844 rattus norv
20	192.5	39.6	99	1 SY07_HUMAN	P80098 homo sapien
21	185.5	38.2	148	1 SY02_MOUSE	P10148 mus musculu
22	184	37.9	120	1 SY16_HUMAN	O15467 h small ind
23	183.5	37.8	120	1 SY02_CAVPO	Q08782 cavia porce
24	180.5	37.1	99	1 SY02_PIG	P42831 sus scrofa
25	179.5	36.9	97	1 EOTA_HUMAN	P51671 homo sapien
26	176.5	36.3	97	1 EOTA_RAT	P97545 rattus norv
27	174.5	35.9	99	1 SY08_HUMAN	P80075 homo sapien
28	174.5	35.9	125	1 SY02_RABIT	P28292 oryctolagus
29	172.5	35.5	94	1 SY26_HUMAN	Q9y258 homo sapien
30	172.5	35.5	99	1 MCPA_BOVIN	P28291 bos taurus
31	172.5	35.5	99	1 SY02_HUMAN	P13500 homo sapien
32	172.5	35.5	99	1 SY02_MACFA	Q9myr4 macaca fasc
33	170	35.0	120	1 SY23_HUMAN	P55773 homo sapien

34	168.5	34.7	97	1 EOTA_MOUSE	P48298 mus musculu
35	167.5	34.5	99	1 SY08_PIG	P49873 sus scrofa
36	166.5	34.3	99	1 SY08_BOVIN	Q09141 bos taurus
37	166.5	34.3	113	1 SY15_HUMAN	Q16663 homo sapien
38	164.5	33.8	94	1 VMI2_KSHV	Q98157 kaposi's sa
39	164.5	33.8	101	1 SY02_CANFA	P52203 canis famil
40	161	33.1	96	1 EOTA_CAVPO	P80325 cavia porce
41	156	32.1	70	1 REG1_BOVIN	P82943 bos taurus
42	152.5	31.4	119	1 SY24_MOUSE	Q9jkc0 mus musculu
43	150.5	31.0	119	1 SY24_HUMAN	O00175 homo sapien
44	146.5	30.1	97	1 SY07_MOUSE	Q03366 mus musculu
45	146.5	30.1	97	1 SY08_MOUSE	Q9z121 mus musculu

ALIGNMENTS

RESULT 1	SY04_HUMAN	SY04_HUMAN	STANDARD;	PRT;	92 AA.
ID	SY04_HUMAN	SY04_HUMAN	STANDARD;	PRT;	92 AA.
AC	P13236; P22617; Q13704;				
DT	01-JAN-1990 (Rel. 13, Created)				
DT	01-JAN-1990 (Rel. 13, Last sequence update)				
DT	15-SEP-2003 (Rel. 42, Last annotation update)				
DE	Small inducible cytokine A4 precursor (CCL4) (Macrophage inflammatory protein 1-beta) (MIP-1-beta) (T-cell activation protein 2) (ACT-2) (PAT 744) (H400) (SIS-gamma) (Lymphocyte activation gene-1 protein) (LAG-1) (HC21) (G-26 T lymphocyte-secreted protein).				
DE	CCL4 OR SCYA4 OR MIP1B OR LAG1.				
GN	Homo sapiens (Human).				
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=89071764; PubMed=2462251;				
RA	Lipes M.A., Napolitano M., Jeang K.-T., Chang N.T., Leonard W.J.;				
RT	"Identification, cloning, and characterization of an immune activation gene."				
RL	Proc. Natl. Acad. Sci. U.S.A. 85:9704-9708(1988).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=89140347; PubMed=2521882;				
RA	Zipfel P.F., Balke J., Irving S.G., Kelly K., Siebenlist U.;				
RT	"Mitogenic activation of human T cells induces two closely related genes which share structural similarities with a new family of secreted factors."				
RL	J. Immunol. 142:1582-1590(1989).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=89093958; PubMed=2521353;				
RA	Brown K.D., Zurawski S.M., Mosmann T.R., Zurawski G.;				
RT	"A family of small inducible proteins secreted by leukocytes are members of a new superfamily that includes leukocyte and fibroblast-derived inflammatory agents, growth factors, and indicators of various activation processes."				
RL	J. Immunol. 142:679-687(1989).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=91061800; PubMed=2247088;				
RA	Baixeras E., Roman-Roman S., Jitsukawa S., Genevee C., Mechiche S., Viegas-Pequignot E., Hercend T., Triebel F.;				
RT	"Cloning and expression of a lymphocyte activation gene (LAG-1)."				
RL	Mol. Immunol. 27:1091-1102(1990).				
RN	[5]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=T-cell;				
RX	MEDLINE=89325421; PubMed=2568930;				
RA	Chang H.C., Reinherz E.L.;				
RT	"Isolation and characterization of a cDNA encoding a putative cytokine which is induced by stimulation via the CD2 structure on human T lymphocytes."				
RL	Eur. J. Immunol. 19:1045-1051(1989).				



[6] SEQUENCE FROM N.A.  
MEDLINE=91373378; PubMed=1894635;  
Napolitano M., Modi W.S., Cevario S.J., Gnarr J.R., Seunanez H.N.,  
Leonard W.J.;  
"The gene encoding the Act-2 cytokine. Genomic structure, HTLV-I/Tax  
responsiveness of 5' upstream sequences, and chromosomal  
localization.";  
J. Biol. Chem. 266:17531-17536(1991).  
[7] SEQUENCE FROM N.A.  
Birren B., Fasman K., McKernan K., Nusbaum C., Richardson P.,  
Lander E.;  
Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
[8] SEQUENCE OF 6-92 FROM N.A.  
MEDLINE=90038522; PubMed=2809212;  
Miller M.D., Hata S., Waal Malefyt R., Krangel M.S.;  
"A novel polypeptide secreted by activated human T lymphocytes.";  
J. Immunol. 143:2907-2916(1989).  
[9] RECEPTOR INTERACTION.  
MEDLINE=98180363; PubMed=9521068;  
Bernardini G., Hedrick J., Sozzani S., Luini W., Spinetti G.,  
Weiss M., Menon S., Zlotnik A., Mantovani A., Santoni A.,  
Napolitano M.;  
"Identification of the CC chemokines TARC and macrophage inflammatory  
protein-1 beta as novel functional ligands for the CCR8 receptor.";  
Eur. J. Immunol. 28:582-588(1998).  
[10] FUNCTION.  
MEDLINE=96106406; PubMed=8525373;  
Cocchi F., DeVico A.L., Garzino-Demo A., Arya S.K., Gallo R.C.,  
Lusso P.;  
"Identification of RANTES, MIP-1 alpha, and MIP-1 beta as the major  
HIV-suppressive factors produced by CD8+ T cells.";  
Science 270:1811-1815(1995).  
[11] STRUCTURE BY NMR.  
MEDLINE=94182137; PubMed=8134838;  
Lodi P.J., Garrett D.S., Kuczewski J., Tsang M.L.S., Weatherbee J.A.,  
Leonard W.J., Gronenborn A.M., Clore G.M.;  
"High-resolution solution structure of the beta chemokine hMIP-1 beta  
by multidimensional NMR.";  
Science 263:1762-1767(1994).  
-!- FUNCTION: MONOKINE WITH INFLAMMATORY AND CHEMOKINETIC PROPERTIES.  
BINDS TO CCR5 AND TO CCR8. ONE OF THE MAJOR HIV-SUPPRESSIVE  
FACTORS PRODUCED BY CD8+ T CELLS. RECOMBINANT MIP-1-BETA INDUCES A  
DOSE-DEPENDENT INHIBITION OF DIFFERENT STRAINS OF HIV-1, HIV-2,  
AND SIMIAN IMMUNODEFICIENCY VIRUS (SIV).  
-!- SUBUNIT: Homodimer.  
-!- SUBCELLULAR LOCATION: Secreted.  
-!- INDUCTION: By mitogens.  
-!- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE  
C-C) (CHEMOKINE CC).  
-----  
This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
modified and this statement is not removed. Usage by and for commercial  
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
EMBL; M23502; AAA36656.1; -  
EMBL; M25316; AAA57256.1; -  
EMBL; J04130; AAA51576.1; -  
EMBL; X53683; CAA37723.1; -  
EMBL; X53682; CAA37722.2; ALT\_SEQ.  
EMBL; X16166; CAA34291.1; -  
EMBL; M6203; AAB00790.1; -  
EMBL; M6201; AAB00790.1; JOINED.  
EMBL; M6202; AAB00790.1; JOINED.

DR EMBL; AC003976; -; NOT\_ANNOTATED\_CDS.  
DR EMBL; M57503; AAA36752.1; -.  
DR PIR; JH0319; A31767.  
DR PDB; 1HUM; 30-APR-94.  
DR PDB; 1HUN; 30-APR-94.  
DR PDB; 1JE4; 03-OCT-01.  
DR Genew; HGNC:10630; CCL4.  
DR MIM; 182284; -.  
DR GO; GO:0005615; C:extracellular space; TAS.  
DR GO; GO:0008009; F:chemokine activity; TAS.  
DR GO; GO:0004716; F:receptor signaling protein tyrosine kinase . . . ; TAS.  
DR GO; GO:0007155; P:cell adhesion; TAS.  
DR GO; GO:0008151; P:cell growth and/or maintenance; TAS.  
DR GO; GO:0006928; P:cell motility; TAS.  
DR GO; GO:0007267; P:cell-cell signaling; TAS.  
DR GO; GO:0007163; P:establishment and/or maintenance of cell po. . . ; TAS.  
DR GO; GO:0006955; P:immune response; TAS.  
DR GO; GO:0006954; P:inflammatory response; TAS.  
DR GO; GO:0009615; P:response to viruses; TAS.  
DR GO; GO:0007165; P:signal transduction; TAS.  
DR GO; GO:0008166; P:viral replication; TAS.  
DR InterPro; IPR000827; CC\_chemokine\_sml.  
DR InterPro; IPR001811; Chemokine\_IL8.  
DR Pfam; PF00048; IL8; 1.  
DR SMART; SM00199; SCY; 1.  
DR PROSITE; PS00472; SMALL\_CYTOKINES\_CC; 1.  
KW Cytokine; Chemotaxis; Inflammatory response; Signal; 3D-structure.  
FT SIGNAL 1 23 SMALL INDUCIBLE CYTOKINE A4.  
FT CHAIN 24 92 BY SIMILARITY.  
FT DISULFID 34 58 BY SIMILARITY.  
FT DISULFID 35 74 T -> C (IN REF. 7).  
FT CONFLICT 6 6 A -> S (IN REF. 6).  
FT CONFLICT 15 15 P -> L (IN REF. 2).  
FT CONFLICT 20 20 ARKLPR -> REASS (IN REF. 3).  
FT CONFLICT 40 45 S -> I (IN REF. 8).  
FT CONFLICT 56 56 S -> G (IN REF. 6).  
FT CONFLICT 70 70 S -> T (IN REF. 7 AND 8).  
FT CONFLICT 80 80  
FT STRAND 29 29  
FT STRAND 33 33  
FT HELIX 45 47  
FT STRAND 50 53  
FT STRAND 63 66  
FT STRAND 72 75  
FT TURN 77 78  
FT HELIX 80 92  
SQ SEQUENCE 92 AA; 10212 MW; F2EA7CF341B0E258 CRC64;  
Query Match 100.0%; Score 486; DB 1; Length 92;  
Best local Similarity 100.0%; Pred. No. 6.1e-47;  
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKLCVTVLSLLMLVAAFCSPPALSAPMGSDPPTACCFSTARKLPNFVVDYETSSLC SQ 60  
Db 1 MKLCVTVLSLLMLVAAFCSPPALSAPMGSDPPTACCFSTARKLPNFVVDYETSSLC SQ 60  
QY 61 PAVVFQTKRSKQVCADPSESWSVQEVYVDLELN 92  
Db 61 PAVVFQTKRSKQVCADPSESWSVQEVYVDLELN 92  
RESULT 2  
SY04\_RABIT  
ID SY04\_RABIT STANDARD; PRT; 92 AA.  
AC P46632;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Small inducible cytokine A4 precursor (CCL4) (Macrophage inflammatory  
protein 1-beta) (MIP-1-beta) (Immune activation protein 2) (ACT-2).  
GN CCL4 OR SCYA4.  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
NCBI\_TaxID=9986;  
[1]  
SEQUENCE FROM N.A.  
STRAIN=New Zealand white;  
MEDLINE=94198229; PubMed=8148323;  
Mori S., Goto K., Goto F., Mutakami K., Ohkawara S., Yoshinaga M.;  
"Dynamic changes in mRNA expression of neutrophils during the course  
of acute inflammation in rabbits.";  
Int. Immunol. 6:149-156(1994).  
-!- FUNCTION: MONOKINE WITH INFLAMMATORY AND CHEMOKINETIC PROPERTIES  
(BY SIMILARITY).  
-!- SUBUNIT: Homodimer (By similarity).  
-!- SUBCELLULAR LOCATION: Secreted.  
-!- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE  
C-C) (CHEMOKINE CC).  
-----  
This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
modified and this statement is not removed. Usage by and for commercial  
entities requires a license agreement (See <http://www.isb-sib.ch>/announce/  
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
EMBL; D17402; BAA04226.1; -.  
PIR; I46730; I46730.  
HSSP; P13236; IHUM.  
InterPro; IPR000827; CC\_chemkine\_sml.  
InterPro; IPR001811; Chemokine\_IL8.  
Pfam; PF00048; IL8; 1.  
SMART; SM00199; SCY; 1.  
PROSITE; PS00472; SMALL\_CYTOKINES\_CC; 1.  
Cytokine; Chemotaxis; Inflammatory response; Signal.  
SIGNAL 1 23 BY SIMILARITY.  
CHAIN 24 92 SMALL INDUCIBLE CYTOKINE A4.  
DISULFID 34 58 BY SIMILARITY.  
DISULFID 35 74 BY SIMILARITY.  
SEQUENCE 92 AA; 10066 MW; ECBA8818D42A735C CRC64;  
-----  
Query Match 84.2%; Score 409; DB 1; Length 92;  
Best Local Similarity 82.6%; Pred. No. 1.9e-38;  
Matches 76; Conservative 9; Mismatches 7; Indels 0; Gaps 0;  
-----  
1 MKLCVTVLSLLMLVAALCPALSPALSGDPTACCFSTYARKLPNRFVVDYETSSLCSSQ 60  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
1 MKLGVTVLSVALLVAALCPPALSPALSGDPTACCFSTYLRKLPNRFVIDYFETSSLCSSQ 60  
-----  
61 PAVVFQTKRSKQVCADPSESQVQYVVDLELN 92  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
61 PAWFQTKRQVCAVNPSESQVQYVVDLELN 92  
-----  
ESULT 3  
Y04 RAT  
D SY04 RAT STANDARD; PRT; 92 AA.  
C P50230;  
T 01-OCT-1996 (Rel. 34, Created)  
T 01-OCT-1996 (Rel. 34, Last sequence update)  
T 28-FEB-2003 (Rel. 41, Last annotation update)  
E Small inducible cytokine A4 precursor (CCL4) (Macrophage inflammatory  
protein 1-beta) (MIP-1-beta).  
N CCL4 OR SCYA4 OR MIP1B.  
S Rattus norvegicus (Rat).  
S Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
C Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
X NCBI\_TaxID=10116;  
N [1]  
P SEQUENCE FROM N.A.  
C STRAIN=Long Evans; TISSUE=Lung;  
A Jones M.L., Shanley T.P., Schmal H., Friedl H.P., Ward P.A.;  
L Submitted (FEB-1994) to the EMBL/GenBank/DBJ databases.  
C -!- FUNCTION: MONOKINE WITH INFLAMMATORY AND CHEMOKINETIC PROPERTIES.

CC -!- SUBUNIT: Homodimer (By similarity).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE  
C-C) (CHEMOKINE CC).  
-----  
This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
modified and this statement is not removed. Usage by and for commercial  
entities requires a license agreement (See <http://www.isb-sib.ch>/announce/  
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
EMBL; U06434; AAA96497.1; -.  
HSSP; P13236; IHUM.  
InterPro; IPR000827; CC\_chemkine\_sml.  
InterPro; IPR001811; Chemokine\_IL8.  
Pfam; PF00048; IL8; 1.  
SMART; SM00199; SCY; 1.  
PROSITE; PS00472; SMALL\_CYTOKINES\_CC; 1.  
Cytokine; Chemotaxis; Inflammatory response; Signal.  
SIGNAL 1 23 BY SIMILARITY.  
CHAIN 24 92 SMALL INDUCIBLE CYTOKINE A4.  
DISULFID 34 58 BY SIMILARITY.  
DISULFID 35 74 BY SIMILARITY.  
SEQUENCE 92 AA; 10234 MW; 60B451EEBEC7103D CRC64;  
-----  
Query Match 81.1%; Score 394; DB 1; Length 92;  
Best Local Similarity 77.2%; Pred. No. 8.6e-37;  
Matches 71; Conservative 10; Mismatches 11; Indels 0; Gaps 0;  
-----  
QY 1 MKLCVTVLSLLMLVAALCPALSPALSGDPTACCFSTYARKLPNRFVVDYETSSLCSSQ 60  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 1 MKLCVSASFSLLLVAALFCDVLSAPIGSDPTSCCFSTYSRKIHRNFVMDYETSSLCSSQ 60  
-----  
QY 61 PAVVFQTKRSKQVCADPSESQVQYVVDLELN 92  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 61 PAVVLTKKGRQICADPSEPWPVWVNDLELN 92  
-----  
RESULT 4  
SY04 MOUSE  
ID SY04 MOUSE STANDARD; PRT; 92 AA.  
AC P14097;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Small inducible cytokine A4 precursor (CCL4) (Macrophage inflammatory  
protein 1-beta) (MIP-1-beta) (H400 protein) (SIS-gamma) (ACT2).  
GN CCL4 OR SCYA4 OR MIP1B.  
OS Mus musculus (Mouse)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89067830; PubMed=3058856;  
RA Sherry B., Tekamp-Olson P., Gallegos C., Bauer D., Davatelis G.,  
RA Wolpe S.D., Maslarsz F., Coit D., Cerami A.;  
RT "Resolution of the two components of macrophage inflammatory protein  
1, and cloning and characterization of one of those components,  
RT macrophage inflammatory protein 1 beta.";  
RL J. Exp. Med. 168:2251-2259(1988).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89093958; PubMed=2521353;  
RA Brown K.D., Zurawski S.M., Mosmann T.R., Zurawski G.;  
RT "A family of small inducible proteins secreted by leukocytes are  
RT members of a new superfamily that includes leukocyte and fibroblast-  
RT derived inflammatory agents, growth factors, and indicators of various  
RT activation processes.";  
RL J. Immunol. 142:679-687(1989).  
RN [3]

SEQUENCE FROM N.A.  
STRAIN=BA/2J; TISSUE=Liver;  
Daubersies P., Lepretre F., Bailleul B., Grove M., Pragnell I.,  
Plumb M.A.;  
Submitted (OCT-1991) to the EMBL/GenBank/DBJ databases.  
[4]  
SEQUENCE FROM N.A.  
STRAIN=B10.S/J, and SJL/J; TISSUE=Spleen;  
MEDLINE=99370037; PubMed=10438970;  
Teuscher C., Butterfield R.J., Ma R.Z., Zachary J.F., Doerge R.W.,  
Blankenhorn E.P.;  
"Sequence polymorphisms in the chemokines Scya1 (TCA-3), Scya2  
(monocyte chemoattractant protein (MCP)-1), and Scya12 (MCP-5) are  
candidates for eae7, a locus controlling susceptibility to monophasic  
remitting/nonrelapsing experimental allergic encephalomyelitis."  
J. Immunol. 163:2262-2266(1999).  
-!- FUNCTION: MONOKINE WITH INFLAMMATORY AND CHEMOKINETIC PROPERTIES.  
-!- SUBUNIT: Homodimer (By similarity).  
-!- SUBCELLULAR LOCATION: Secreted.  
-!- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE  
C-C) (CHEMOKINE CC).  
-----  
This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
modified and this statement is not removed. Usage by and for commercial  
entities requires a license agreement (See [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/)  
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
EMBL; M23503; AAA40148.1; -  
EMBL; M35590; AAA39708.1; -  
EMBL; X62502; CAA44364.1; -  
EMBL; AF128218; AAF22559.1; -  
EMBL; AF128219; AAF22560.1; -  
PIR; C30552; C30552.  
HSSP; P13236; IHUM.  
MGD; MGI:98261; CC14.  
InterPro; IPR000827; CC\_chemokine\_sml.  
InterPro; IPR001811; Chemokine\_IL8.  
Pfam; PF00048; IL8; 1.  
SMART; SM00199; SCY; 1.  
PROSITE; PS00472; SMALL\_CYTOKINES\_CC; 1.  
Cytokine; Chemotaxis; Inflammatory response; Signal.  
T SIGNAL 1 23 SMALL INDUCIBLE CYTOKINE A4.  
CHAIN 24 92  
DISULFID 34 58 BY SIMILARITY.  
DISULFID 35 74 BY SIMILARITY.  
T Q SEQUENCE 92 AA; 10168 MW; 8853FD58FDE61BAC CRC64;  
-----  
Query Match 80.2%; Score 390; DB 1; Length 92;  
Best Local Similarity 76.1%; Pred. No. 2.4e-36;  
Matches 70; Conservative 13; Mismatches 9; Indels 0; Gaps 0;  
Y 1 MKLCVTLSLLMLVAFCSPALSGDPTACCFSTYARKLPNRFVVDYETSSLCSSQ 60  
b 1 MKLCVSALSLLLVAAFCAPGFSAPMGSDPTSCCFSTYRQLHRSFVMDYETSSLCSSK 60  
Y 61 PAVVFQTKRSKQVCADPSESNVQYVYDLELN 92  
b 61 PAVVFLTKRGRQICANPSEPWPVYMSDLELN 92  
-----  
RESULT 5  
Y03 MOUSE  
D -SY03 MOUSE STANDARD; PRT; 92 AA.  
C P10855; P14096;  
Y 01-JUL-1989 (Rel. 11, Created)  
Y 01-APR-1990 (Rel. 14, Last sequence update)  
Y 15-SEP-2003 (Rel. 42, Last annotation update)  
E Small inducible cytokine A3 precursor (CCL3) (Macrophage inflammatory  
protein 1-alpha) (MIP-1-alpha) (TY-5) (SIS-alpha) (Heparin-binding  
chemotaxis protein) (L2G25B).  
-----

GN CCL3 OR SCYA3 OR MIP1A.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88258380; PubMed=3290382;  
RA Davatelis G., Tekamp-Olson P., Wolpe S.D., Hermesen K., Luedke C.,  
Gallegos C., Coit D., Merryweather J., Cerami A.;  
RT "Cloning and characterization of a cDNA for murine macrophage  
inflammatory protein (MIP), a novel monokine with inflammatory and  
chemokinetic properties."  
J. Exp. Med. 167:1939-1944(1988).  
RN [2]  
RP REVISIONS.  
RA Davatelis G., Tekamp-Olson P., Wolpe S.D., Hermesen K., Luedke C.,  
Gallegos C., Coit D., Merryweather J., Cerami A.;  
RL J. Exp. Med. 170:2189-2189(1989).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89093958; PubMed=2521353;  
RA Brown K.D., Zurawski S.M., Mosmann T.R., Zurawski G.;  
RT "A family of small inducible proteins secreted by leukocytes are  
members of a new superfamily that includes leukocyte and  
fibroblast-derived inflammatory agents, growth factors, and  
indicators of various activation processes."  
J. Immunol. 142:679-687(1989).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BA/2J;  
RX MEDLINE=91016858; PubMed=2216738;  
RA Grove M., Lowe S., Graham G., Pragnell I., Plumb M.;  
RT "Sequence of the murine haemopoietic stem cell inhibitor/macrophage  
inflammatory protein 1 alpha gene."  
Nucleic Acids Res. 18:5561-5561(1990).  
RN [5]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89184547; PubMed=2784565;  
RA Kwon B.S., Weissman S.M.;  
RT "cDNA sequences of two inducible T-cell genes."  
Proc. Natl. Acad. Sci. U.S.A. 86:1963-1967(1989).  
RN [6]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91237116; PubMed=2033269;  
RA Widmer U., Yang Z., van Deventer S., Manogue K.R., Sherry B.,  
Cerami A.;  
RT "Genomic structure of murine macrophage inflammatory protein-1 alpha  
and conservation of potential regulatory sequences with a human  
homolog, Lp78."  
J. Immunol. 146:4031-4040(1991).  
RN [7]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BA/2J, DBA/2J, NOD/LTJ, SJL/J, and B10.S/J; TISSUE=Spleen;  
RX MEDLINE=99370037; PubMed=10438970;  
RA Teuscher C., Butterfield R.J., Ma R.Z., Zachary J.F., Doerge R.W.,  
Blankenhorn E.P.;  
RT "Sequence polymorphisms in the chemokines Scya1 (TCA-3), Scya2  
(monocyte chemoattractant protein (MCP)-1), and Scya12 (MCP-5) are  
candidates for eae7, a locus controlling susceptibility to monophasic  
remitting/nonrelapsing experimental allergic encephalomyelitis."  
J. Immunol. 163:2262-2266(1999).  
RN [8]  
RP SEQUENCE OF 24-42.  
RX MEDLINE=88154745; PubMed=3279154;  
RA Wolpe S.D., Davatelis G., Sherry B., Beutler B., Hesse D.G.,  
Nguyen H.T., Moldaver L.L., Nathan C.F., Lowry S.F., Cerami A.;  
RT "Macrophages secrete a novel heparin-binding protein with  
inflammatory and neutrophil chemokinetic properties."  
J. Exp. Med. 167:570-581(1988).  
CC -!- FUNCTION: MONOKINE WITH INFLAMMATORY, PYROGENIC AND CHEMOKINETIC  
CC PROPERTIES. HAS A POTENT CHEMOTACTIC ACTIVITY FOR EOSINOPHILS.  
CC BINDING TO A HIGH-AFFINITY RECEPTOR ACTIVATES CALCIUM RELEASE IN









SEQUENCE FROM N.A.  
MEDLINE=91103879; PubMed=2271120;  
Blum S., Forsdyke R.E., Forsdyke D.R.;  
"Three human homologs of a murine gene encoding an inhibitor of stem  
cell proliferation.";  
DNA Cell Biol. 9:589-602(1990).  
[4]  
SEQUENCE FROM N.A.  
MEDLINE=90287155; PubMed=1694014;  
Nakao M., Nomiya H., Shimada K.;  
"Structures of human genes coding for cytokine LD78 and their  
expression.";  
Mol. Cell. Biol. 10:3646-3658(1990).  
[5]  
SEQUENCE OF 23-92 FROM N.A.  
Jang J.S., Kim B.E.;  
Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
[6]  
SEQUENCE OF 24-92, AND MUTAGENESIS OF ASP-49.  
MEDLINE=96127782; PubMed=8541527;  
Hunter M.G., Bawden L., Brotherton D., Craig S., Cribbes S.,  
Czaplewski L.G., Dexter T.M., Drummond A.H., Gearing A.H.,  
Heyworth C.M., Lord B.I., McCourt M., Varley P.G., Wood L.M.,  
Edwards R.M., Lewis P.J.;  
"BB-10010: an active variant of human macrophage inflammatory protein-  
1 alpha with improved pharmaceutical properties.";  
Blood 86:4400-4408(1995).  
[7]  
SEQUENCE OF 27-40 AND 71-83, AND FUNCTION.  
MEDLINE=96106406; PubMed=8525373;  
Cocchi F., DeVico A.L., Garzino-Demo A., Arya S.K., Gallo R.C.,  
Lusso P.;  
"Identification of RANTES, MIP-1 alpha, and MIP-1 beta as the major  
HIV-suppressive factors produced by CD8+ T cells.";  
Science 270:1811-1815(1995).  
-!- FUNCTION: MONOKINE WITH INFLAMMATORY AND CHEMOKINETIC PROPERTIES.  
BINDS TO CCRL, CCR4 AND CCR5. ONE OF THE MAJOR HIV-SUPPRESSIVE  
FACTORS PRODUCED BY CD8+ T CELLS. RECOMBINANT MIP-1-ALPHA INDUCES  
A DOSE-DEPENDENT INHIBITION OF DIFFERENT STRAINS OF HIV-1, HIV-2,  
AND SIMIAN IMMUNODEFICIENCY VIRUS (SIV).  
-!- SUBCELLULAR LOCATION: Secreted.  
-!- INDUCTION: BY TPA OR PHA (TPA = 12-O-TETRADECANOYL PHORBOL-13  
ACETATE (TUMOR PROMOTER); PHA = PHYTOHEMAGGLUTININ (T-CELL  
MITOGEN)).  
-!- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE  
C-C) (CHEMOKINE CC). STRONG, TO SCYA3L1.  
-----  
This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
modified and this statement is not removed. Usage by and for commercial  
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
EMBL; D00044; BAA00029.1; -  
EMBL; M23452; AAA36316.1; -  
EMBL; M25315; AAA57255.1; -  
EMBL; X03754; CAA27388.1; -  
EMBL; X04018; CAA27643.1; ALT\_SEQ.  
EMBL; M23178; AAA35858.1; -  
EMBL; D90144; BAA14172.1; -  
EMBL; AF043339; AAC03539.1; -  
PIR; A35673; A30574.  
PDB; 1B50; 22-JUL-99.  
PDB; 1B53; 22-JUL-99.  
Genew; HGNC:10627; CCL3.  
MIM; 182283; -  
GO; GO:0005625; C:soluble fraction; TAS.  
GO; GO:0003800; F:antiviral response protein activity; TAS.  
GO; GO:0008009; F:chemokine activity; TAS.  
GO; GO:0004871; F:signal transducer activity; TAS.  
GO; GO:0006961; P:antibacterial humoral response (sensu Inver. . .; TAS.

DR GO:0006874; P:calcium ion homeostasis; TAS.  
DR GO:0006928; P:cell motility; TAS.  
DR GO:0007267; P:cell-cell signaling; TAS.  
DR GO:0006935; P:chemotaxis; TAS.  
DR GO:0006887; P:exocytosis; TAS.  
DR GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.  
DR GO:0006955; P:immune response; TAS.  
DR GO:0006954; P:inflammatory response; TAS.  
DR GO:0007011; P:regulation of cytoskeleton; TAS.  
DR GO:0007165; P:signal transduction; TAS.  
DR GO:0008166; P:viral replication; TAS.  
DR InterPro; IPR000827; CC chemokine sml.  
DR InterPro; IPR001811; Chemokine\_IL8.  
DR Pfam; PF00048; IL8; 1.  
DR SMART; SM00199; SCY; 1.  
DR PROSITE; PS00472; SMALL CYTOKINES\_CC; 1.  
KW Cytokine; Chemotaxis; Inflammatory response; Signal; 3D-structure.  
FT SIGNAL 1 23  
FT CHAIN 24 92 SMALL INDUCIBLE CYTOKINE A3.  
FT DISULFID 33 57 BY SIMILARITY.  
FT DISULFID 34 73 BY SIMILARITY.  
FT MUTAGEN 49 49 D->A: IN BB-10010; IMPROVED  
FT PHARMACEUTICAL PROPERTIES.  
SQ SEQUENCE 92 AA; 10085 MW; 517865D5D676CA8 CRC64;  
Query Match 61.8%; Score 300.5; DB 1; Length 92;  
Best Local Similarity 57.6%; Pred. No. 1.8e-26;  
Matches 53; Conservative 19; Mismatches 19; Indels 1; Gaps 1;  
Qy 1 MKLCVTVLSLLMLVAFCSPALSPMGSDPPACCFSTYARKLPNFVVDYETSSLCQ 60  
Db 1 MQVSTAALAVLLCTMALCN-QFSASLAADTPACCFSTYRSQIPQNFIAFYFETSSQCSK 59  
Qy 61 PAVVFQTKRSKQVCADPSESQVQYVVDLELN 92  
Db 60 PGVIFLTRSRQVCADPSEEWQYVVDLELS 91  
RESULT 9  
SY04 CHICK  
ID SY04 CHICK STANDARD; PRT; 90 AA.  
AC Q90826; Q910C9;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Small inducible cytokine A4 homolog precursor (Macrophage inflammatory  
protein 1-beta homolog).  
DE CCL4 OR SCYA4.  
GN Gallus gallus (Chicken).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Bone marrow;  
RX MEDLINE=95369710; PubMed=7642115;  
RA Petrenko O., Ischenko I., Enrietto P.J.;  
RT "Isolation of a cDNA encoding a novel chicken chemokine homologous to  
mammalian macrophage inflammatory protein-1 beta.";  
RL Gene 160:305-306(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Hughes S.M., Bumstead N.;  
RT "Mapping of the gene encoding the chicken homologue of the mammalian  
chemokine SCYA4.";  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE OF 14-90 FROM N.A.  
RA Petrenko O., Enrietto P.J.;  
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: MONOKINE WITH INFLAMMATORY AND CHEMOKINETIC PROPERTIES  
CC (BY SIMILARITY).





MEDLINE=22388257; PubMed=12477932;  
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
Bosak S.A., McEwan P.K., McKernan K.J., Malek J.A., Gunaratne P.H.,  
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
Fahey J., Helton E., Kettman M., Madan A.C., Shevchenko Y., Bouffard G.G.,  
Whiting M., Touchman J.W., Green E.D., Dickson M.C.,  
Blakesley R.W., Grimwood J., Schmutz J., Myers R.M.,  
Rodriguez A.C., Rodriguez J., Skalska U., Smailus D.E.,  
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
"Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences";  
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[6]  
SEQUENCE OF 49-56; 71-79 AND 83-91, AND FUNCTION.  
MEDLINE=96106406; PubMed=8525373;  
Cocchi F., DeVico A.L., Garzino-Demo A., Arya S.K., Gallo R.C.,  
Lusso P.;  
"Identification of RANTES, MIP-1 alpha, and MIP-1 beta as the major  
HIV-suppressive factors produced by CD8+ T cells";  
Science 270:1811-1815(1995).  
[7]  
STRUCTURE BY NMR.  
MEDLINE=95352612; PubMed=7542919;  
Chung C.-W., Cooke R.M., Proudfoot A.E.I., Wells T.N.C.;  
"The three-dimensional solution structure of RANTES";  
Biochemistry 34:9307-9314(1995).  
[8]  
STRUCTURE BY NMR.  
MEDLINE=95244456; PubMed=7537088;  
Skelton N.J., Aspiras F., Ogez J., Schall T.J.;  
"Proton NMR assignments and solution conformation of RANTES, a  
chemokine of the C-C type";  
Biochemistry 34:5329-5342(1995).  
[9]  
SYNTHESIS, AND X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).  
MEDLINE=99111238; PubMed=9889151;  
Wilken J., Hoover D., Thompson D.A., Barlow P.N., McSparron H.,  
Picard L., Wlodawer A., Lubkowski J., Kent S.B.;  
"Total chemical synthesis and high-resolution crystal structure of  
the potent anti-HIV protein AOP-RANTES";  
Chem. Biol. 6:43-51(1999).  
[10]  
X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).  
Hoover D.M., Shaw J., Gryczynski Z., Proudfoot A.E.I., Wells T.N.C.,  
Lubkowski J.;  
"The crystal structure of Met-RANTES: comparison with native RANTES  
and AOP-RANTES";  
Protein Pept. Lett. 7:73-82(2000).  
-!- FUNCTION: CHEMOATTRACTANT FOR BLOOD MONOCYTES, MEMORY T HELPER  
CELLS AND EOSINOPHILS. CAUSES THE RELEASE OF HISTAMINE FROM  
BASOPHILS AND ACTIVATES EOSINOPHILS. BINDS TO CCR1, CCR3, CCR4 AND  
CCR5. ONE OF THE MAJOR HIV-SUPPRESSIVE FACTORS PRODUCED BY CD8+ T  
CELLS. RECOMBINANT RANTES PROTEIN INDUCES A DOSE-DEPENDENT  
INHIBITION OF DIFFERENT STRAINS OF HIV-1, HIV-2, AND SIMIAN  
IMMUNODEFICIENCY VIRUS (SIV).  
-!- SUBCELLULAR LOCATION: Secreted.  
-!- TISSUE SPECIFICITY: T-CELL AND MACROPHAGE SPECIFIC.  
-!- INDUCTION: By mitogens.  
-!- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE  
C-C) (CHEMOKINE CC).  
-----  
This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
CC EMBL; M21121; AAA36725.1; -  
DR EMBL; AF043341; AAC03541.1; -  
DR EMBL; AF088219; AAC63331.1; -  
DR EMBL; AF266753; AAF73070.1; -  
DR EMBL; BC008600; AAH08600.1; -  
DR PIR; A28815; A28815.  
DR PDB; 1HRJ; 14-OCT-96.  
DR PDB; 1RTN; 03-JUN-95.  
DR PDB; 1RTO; 03-JUN-95.  
DR PDB; 1B3A; 23-APR-99.  
DR PDB; 1EQT; 19-APR-00.  
DR Genew; HGNC:10632; CCL5.  
DR MIM; 187011; -  
DR GO; GO:0003800; F:antiviral response protein activity; TAS.  
DR GO; GO:0008009; F:chemokine activity; TAS.  
DR GO; GO:0006874; P:calcium ion homeostasis; TAS.  
DR GO; GO:0007155; P:cell adhesion; TAS.  
DR GO; GO:0006928; P:cell motility; TAS.  
DR GO; GO:0007267; P:cell-cell signaling; TAS.  
DR GO; GO:0006968; P:cellular defense response; TAS.  
DR GO; GO:0006935; P:chemotaxis; TAS.  
DR GO; GO:0006887; P:exocytosis; TAS.  
DR GO; GO:0006954; P:inflammatory response; TAS.  
DR GO; GO:0006979; P:response to oxidative stress; TAS.  
DR GO; GO:0006915; P:response to viruses; TAS.  
DR GO; GO:0007165; P:signal transduction; TAS.  
DR InterPro; IPR000827; CC\_chemokine\_sml.  
DR InterPro; IPR001811; Chemokine\_IL8.  
DR Pfam; PF00048; IL8; 1.  
DR SMART; SM00199; SCY; 1.  
DR PROSITE; PS00472; SMALL\_CYTOKINES\_CC; 1.  
KW Cytokine; Chemotaxis; T-cell; Signal; Inflammatory response;  
KW 3D-structure.  
FT SIGNAL 1 23 SMALL INDUCIBLE CYTOKINE A5.  
FT CHAIN 24 91  
FT DISULFID 33 57  
FT DISULFID 34 73  
FT CONFLICT 7 7  
FT CONFLICT 14 14  
FT STRAND 30 33  
FT HELIX 44 46  
FT STRAND 47 52  
FT TURN 55 56  
FT STRAND 62 66  
FT TURN 67 68  
FT STRAND 71 74  
FT TURN 76 77  
FT HELIX 79 91  
SQ SEQUENCE 91 AA; 9990 MW; FB0BFAF9A87C620F CRC64;  
Query Match 50.5%; Score 245.5; DB 1; Length 91;  
Best Local Similarity 45.7%; Pred. No. 2e-20;  
Matches 42; Conservative 23; Mismatches 26; Indels 1; Gaps 1;  
QY 1 MKLCVTVLSSLMLVAAPCSALSPALMGSDPPPTACCFSTYARKLPNRFVVDYETSSLCSSQ 60  
Db 1 MKVSAALAVILIALCAPASAPSYSSD-TTPCCFAYIARPLPRAHIKEFYFTSGKCSN 59  
QY 61 PAVVFQTKRSKQVCADPSSESWVQEVYDLELN 92  
Db 60 PAVVFVTRKNRQVCANPEKKWVREYINLSLEMS 91  
RESULT 12  
SY05\_MOUSE  
ID SY05\_MOUSE STANDARD; PRT; 91 AA.  
AC P30832;  
DT 01-JUL-1993 (Rel. 26, Created)



01-JUN-1994 (Rel. 29, Last sequence update)  
15-SEP-2003 (Rel. 42, Last annotation update)  
Small inducible cytokine A5 precursor (CCL5) (T-cell specific RANTES protein) (SIS-delta) (MuRantes).  
CCL5 OR SCYAS.  
Mus musculus (Mouse).  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
NCBI\_TaxID=10090;  
[1]  
SEQUENCE FROM N.A.  
MEDLINE=92277990; PubMed=1375672;  
Heeger P., Wolf G., Meyers C., Sun M.J., O'Farrell S.C.,  
Krensky A.M., Neilson E.G.;  
"Isolation and characterization of cDNA from renal tubular epithelium encoding murine Rantes.";  
Kidney Int. 41:220-225(1992).  
[2]  
SEQUENCE FROM N.A.  
MEDLINE=92289805; PubMed=1376260;  
Schall T.J., Simpson N.J., Mak J.Y.;  
"Molecular cloning and expression of the murine RANTES cytokine: structural and functional conservation between mouse and man.";  
Eur. J. Immunol. 22:1477-1481(1992).  
[3]  
SEQUENCE FROM N.A.  
STRAIN=NIH Swiss;  
MEDLINE=94132613; PubMed=7507961;  
Danoff T.M., Lalley P.A., Chang Y.S., Heeger P.S., Neilson E.G.;  
"Cloning, genomic organization, and chromosomal localization of the Scy5 gene encoding the murine chemokine RANTES.";  
J. Immunol. 152:1182-1189(1994).  
[4]  
SEQUENCE FROM N.A.  
STRAIN=BALB/C;  
MEDLINE=94217689; PubMed=7513046;  
Shin H.S., Drysdale B.E., Shin M.L., Noble P.W., Fisher S.N., Paznekas W.A.;  
"Definition of a lipopolysaccharide-responsive element in the 5'-flanking regions of Murantes and crg-2.";  
Mol. Cell. Biol. 14:2914-2925(1994).  
[5]  
SEQUENCE FROM N.A.  
STRAIN=B10.S/J, BALB/CJ, DBA/2J, NOD/LTJ, and SJL/J; TISSUE=Spleen;  
MEDLINE=99370037; PubMed=10438970;  
Teuscher C., Butterfield R.J., Ma R.Z., Zachary J.F., Doerge R.W., Blankenhorn E.P.;  
"Sequence polymorphisms in the chemokines Scy1 (TCA-3), Scy2 (monocyte chemoattractant protein (MCP)-1), and Scy12 (MCP-5) are candidates for eae7, a locus controlling susceptibility to monophasic remitting/nonrelapsing experimental allergic encephalomyelitis.";  
J. Immunol. 163:2262-2266(1999).  
[6]  
SEQUENCE FROM N.A.  
STRAIN=129/Sv;  
Nomiya H.;  
"Organization of the mouse CC chemokine cluster containing the genes for C10, MRP-2 and RANTES.";  
Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
[7]  
SEQUENCE FROM N.A.  
STRAIN=C57BL/6J; TISSUE=Pancreas;  
PubMed=12466851;  
Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S., Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., Blake J.A., Bradt D., Brusica V., Chothia C., Corbani L.E., Cousins S., Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S., Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J., Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D., Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H., Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S., Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C., Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L., Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.;  
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";  
Nature 420:563-573(2002).  
[8]  
SEQUENCE FROM N.A.  
TISSUE=Mammary gland;  
PubMed=12477932;  
Straussberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";  
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
-!- FUNCTION: CHEMOATTRACTANT FOR BLOOD MONOCYTES, MEMORY T HELPER CELLS AND EOSINOPHILS. CAUSES THE RELEASE OF HISTAMINE FROM BASOPHILS AND ACTIVATES EOSINOPHILS.  
-!- SUBCELLULAR LOCATION: Secreted.  
-!- TISSUE SPECIFICITY: T-CELL AND MACROPHAGE SPECIFIC.  
-!- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE C-C) (CHEMOKINE CC).  
-----  
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
EMBL; M77747; AAA40029.1; -  
EMBL; S37648; AAB22330.1; -  
EMBL; U02298; AAA18302.1; -  
EMBL; X70675; CAA50011.1; -  
EMBL; AF065944; AAC17511.1; -  
EMBL; AF065945; AAC17512.1; -  
EMBL; AF065946; AAC17513.1; -  
EMBL; AF065947; AAC17514.1; -  
EMBL; AF128187; AAF22528.1; -  
EMBL; AB051897; BAB18731.1; -  
EMBL; AK003101; BAB22566.1; -  
EMBL; BC033508; AAH33508.1; -  
PIR; I48875; A46539.  
HSSP; PI3501; LRTN.

MGI:98262; Ccl5.  
InterPro; IPR000827; CC\_chemkine\_sml.  
InterPro; IPR001811; Chemokine\_IL8.  
Pfam; PF00048; IL8; 1.  
SMART; SM00199; SCY; 1.  
PROSITE; PS00472; SMALL\_CYTOKINES\_CC; 1.  
Cytokine; Chemotaxis; T-cell; Signal; Inflammatory response.  
SIGNAL 1 23 POTENTIAL.  
CHAIN 24 91 SMALL INDUCIBLE CYTOKINE A5.  
BY SIMILARITY.  
DISULFID 33 57 BY SIMILARITY.  
BY SIMILARITY.  
CONFLICT 34 73 BY SIMILARITY.  
CONFLICT 19 19 T -> A (IN REF. 2).  
CONFLICT 41 41 A -> E (IN REF. 1).  
SEQUENCE 91 AA; 10071 MW; 5DFD66F4684FE1C8 CRC64;  
Query Match 49.9%; Score 242.5; DB 1; Length 91;  
Best Local Similarity 48.9%; Pred. No. 4.4e-20;  
Matches 45; Conservative 20; Mismatches 26; Indels 1; Gaps 1;  
1 MKLCVTVLSLLMLVAFCSPALSPMGSDPPTACCFSTYARKLPNRFVVDYETSSLCQ 60  
1 MKISAAALTIILTAALCTPAPASPYGSD-TTPCCFAYLSLALPRAHVKEYFYTSSKCSN 59  
61 PAVVFQTKRSQKQVCADPSESQVQYVVDLELN 92  
60 LAVVFVTRNRQVCANPEKKVQYINYLEMS 91  
RESULT 13  
SY05\_SIGHI STANDARD; PRT; 91 AA.  
Q91ZL1;  
28-FEB-2003 (Rel. 41, Created)  
28-FEB-2003 (Rel. 41, Last sequence update)  
28-FEB-2003 (Rel. 41, Last annotation update)  
Small inducible cytokine A5 precursor (CCL5) (T-cell specific RANTES protein).  
CCL5 OR SCYA5.  
Sigmodon hispidus (Hispid cotton rat).  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae; Sigmodon.  
NCBI\_TaxID=42415;  
[1]  
SEQUENCE FROM N.A.  
Blanco J.C., Pletneva L.M., Prince G.A.;  
"Sigmodon hispidus cytokines, chemokines and interferons.";  
Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
-!- FUNCTION: CHEMOATTRACTANT FOR BLOOD MONOCYTES, MEMORY T HELPER CELLS AND EOSINOPHILS. CAUSES THE RELEASE OF HISTAMINE FROM BASOPHILS AND ACTIVATES EOSINOPHILS (BY SIMILARITY).  
-!- SUBCELLULAR LOCATION: Secreted.  
-!- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE C-C) (CHEMOKINE CC).  
-----  
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
EMBL; AF421391; AAL16932.1; --  
InterPro; IPR000827; CC\_chemkine\_sml.  
InterPro; IPR001811; Chemokine\_IL8.  
Pfam; PF00048; IL8; 1.  
SMART; SM00199; SCY; 1.  
PROSITE; PS00472; SMALL\_CYTOKINES\_CC; 1.  
Cytokine; Chemotaxis; T-cell; Signal; Inflammatory response.  
SIGNAL 1 23 POTENTIAL.  
CHAIN 24 91 SMALL INDUCIBLE CYTOKINE A5.  
BY SIMILARITY.  
DISULFID 33 57 BY SIMILARITY.

FT DISULFID 34 73 BY SIMILARITY.  
SQ SEQUENCE 91 AA; 10082 MW; D0D6EABE4242FF CRC64;  
Query Match 49.1%; Score 238.5; DB 1; Length 91;  
Best Local Similarity 49.5%; Pred. No. 1.2e-19;  
Matches 45; Conservative 20; Mismatches 25; Indels 1; Gaps 1;  
1 MKLCVTVLSLLMLVAFCSPALSPMGSDPPTACCFSTYARKLPNRFVVDYETSSLCQ 60  
1 MKISAAVLTIVLMAASLCAPASAPNGSD-TIPCCFAYLSAVLPRAHVKEYFYTSSKCSN 59  
61 PAVVFQTKRSQKQVCADPSESQVQYVVDLEL 91  
60 FAVVFVTRNRQVCANPKKKVQYINYLEL 90  
RESULT 14  
SY05\_CAVPO STANDARD; PRT; 91 AA.  
ID SY05\_CAVPO STANDARD; PRT; 91 AA.  
AC P97272; O09076;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Small inducible cytokine A5 precursor (CCL5) (T-cell specific RANTES protein) (SIS-delta).  
DE CCL5 OR SCYA5.  
GN Cavia porcellus (Guinea pig).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.  
OX NCBI\_TaxID=10141;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Dunkin-Hartley;  
RA Campbell E.M., Proudfoot A.E.I., Yoshimura T., Allet B., Wells T.N.C., White A.M., Westwick J., Watson M.L.;  
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RA Asano K., Nakamura M., Oguma T., Fukunaga K., Ishizaka A., Yamaguchi K., Kanazawa M.;  
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: CHEMOATTRACTANT FOR BLOOD MONOCYTES, MEMORY T HELPER CELLS AND EOSINOPHILS. CAUSES THE RELEASE OF HISTAMINE FROM BASOPHILS AND ACTIVATES EOSINOPHILS (BY SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE C-C) (CHEMOKINE CC).  
-----  
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
EMBL; U77037; AAC53293.1; --  
EMBL; AB002662; BAA19604.1; --  
DR HSSP; P13501; IRTN.  
DR InterPro; IPR000827; CC\_chemkine\_sml.  
DR InterPro; IPR001811; Chemokine\_IL8.  
DR Pfam; PF00048; IL8; 1.  
DR SMART; SM00199; SCY; 1.  
DR PROSITE; PS00472; SMALL\_CYTOKINES\_CC; 1.  
KW Cytokine; Chemotaxis; T-cell; Signal; Inflammatory response.  
FT SIGNAL 1 23 POTENTIAL.  
FT CHAIN 24 91 SMALL INDUCIBLE CYTOKINE A5.  
FT DISULFID 33 57 BY SIMILARITY.  
FT DISULFID 34 73 BY SIMILARITY.  
SQ SEQUENCE 91 AA; 10088 MW; 7F6A31B751237DB9 CRC64;  
Query Match 48.3%; Score 234.5; DB 1; Length 91;

Search completed: December 16, 2003, 15:38:21  
Job time : 10.5574 secs

```
Best Local Similarity 45.7%; Pred. No. 3.3e-19;
Matches 42; Conservative 21; Mismatches 28; Indels 1; Gaps 1;

1 MKLCVTVLSLLMLVAACSPALSGMSPPTACCFSTYARKLPNRFVVDYVYETSSLSQ 60
||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||
1 MKVSAALCVILTTAALCVPASASPYASD-TTPCCFAYISRALPRTHIKEYFYTSSKCSN 59
||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||

61 PAVVFQTKRSKQVCADPSESWSVQYVYVDLELN 92
||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||
60 LAVVFVTRKNRQVCANPEKKWVREYINSLEMS 91
||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||

RESULT 15
(05_RAT STANDARD; PRT; 92 AA.
SY05_RAT
P50231;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Small inducible cytokine A5 precursor (CCL5) (T-cell specific RANTES
protein) (SIS-delta).
CCL5 OR SCYA5.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
SEQUENCE FROM N.A. TISSUE=Lung;
STRAIN=Long Evans; Jones M.L., Shanley T.P., Ward P.A.;
Submitted (FEB-1994) to the EMBL/GenBank/DBJ databases.
-!- FUNCTION: CHEMOATTRACTANT FOR BLOOD MONOCYTES, MEMORY T HELPER
CELLS AND EOSINOPHILS. CAUSES THE RELEASE OF HISTAMINE FROM
BASOPHILS AND ACTIVATES EOSINOPHILS (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
C-C) (CHEMOKINE CC).
-----
This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
-----
EMBL; U06436; AAA96499.1; -
HSSP; P13501; IRTN.
InterPro; IPR000827; CC_chemokine_sml.
InterPro; IPR001811; Chemokine_IL8.
Pfam; PF00048; IL8; 1.
SMART; SM00199; SCY; 1.
PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
Cytokine; Chemotaxis; T-cell; Signal; Inflammatory response.
SIGNAL 1 24 POTENTIAL.
CHAIN 25 92 SMALL INDUCIBLE CYTOKINE A5.
DISULFID 34 58 BY SIMILARITY.
DISULFID 35 74 BY SIMILARITY.
SEQUENCE 92 AA; 10170 MW; B4FBE2B4208ABC6 CRC64;

Query Match 47.1%; Score 229; DB 1; Length 92;
Best Local Similarity 47.3%; Pred. No. 1.4e-18;
Matches 44; Conservative 21; Mismatches 26; Indels 2; Gaps 2;

1 MKLCVTV-LSLLMLVAACSPALSGMSPPTACCFSTYARKLPNRFVVDYVYETSSLSQ 59
||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||
1 MKISAAAASLTIVLVAALCTVPASPYSYD-TTPCCFAYLSLALPRAHVKEYFYTSSKCS 59
||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||

60 QPAVVFQTKRSKQVCADPSESWSVQYVYVDLELN 92
||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||
60 NLAVVFVTRNRQVCANPEKKWVQYVYVLEMS 92
||| : : : ||| : : : ||| : : : ||| : : : ||| : : : |||
```

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.  
protein - protein search, using sw model  
n on: December 16, 2003, 15:36:20 ; Search time 30.6667 Seconds  
(without alignments)  
774.158 Million cell updates/sec

US-09-920-137A-7  
rfect score: 486  
quence: 1 MKLCVTVLSLLMLVAAPFCSP.....VCADPSESWVQYVYDLELN 92

oring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
arched: 830525 seqs, 258052604 residues  
tal number of hits satisfying chosen parameters: 830525

nimum DB seq length: 0  
ximum DB seq length: 2000000000  
st-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

tabase : SPTREMBL 23:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriaph:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES					
Result No.	Score	Query Match %	Length DB ID	Description	
1	468	96.3	92 4 Q8NHW4	Q8nhw4 homo sapien	
2	459	94.4	92 6 Q8HYQ2	Q8hyq2 macaca mula	
3	376	77.4	92 11 Q91ZL0	Q91zl0 sigmodon hi	
4	320	65.8	93 6 Q8SQA6	Q8sqa6 bos taurus	
5	294.5	60.6	92 11 Q91Z65	Q91z65 sigmodon hi	
6	281.5	57.9	92 6 Q8HYQ3	Q8hyq3 macaca mula	
7	271.5	55.9	80 4 Q14745	Q14745 homo sapien	
8	264	54.3	90 13 Q9PWA6	Q9pwa6 gallus gall	
9	252	51.9	49 6 Q8HYN3	Q8hyn3 macaca mula	
10	249	51.2	56 6 Q8HYN4	Q8hyn4 macaca mula	
11	245.5	50.5	89 13 Q91BE0	Q91be0 gallus gall	
12	243.5	50.1	91 6 Q8MKD0	Q8mkd0 equus cabal	
13	240.5	49.5	91 6 Q8HYQ1	Q8hyq1 macaca mula	
14	233.5	48.0	91 13 Q8QGS7	Q8qgs7 gallus gall	
15	225.5	46.4	91 6 Q8HYS0	Q8hys0 canis famil	
16	224	46.1	92 6 Q8SQ40	Q8sq40 felis silve	

17	204	42.0	88	6	Q8HYP8	Q8hyp8 macaca mula
18	189.5	39.0	91	13	Q8QGS6	Q8qgs6 gallus gall
19	184.5	38.0	148	11	Q9QYD7	Q9qyd7 mus musculu
20	182	37.4	150	11	Q8CGM5	Q8cgm5 sigmodon hi
21	179.5	36.9	99	6	Q9TTQ3	Q9ttq3 equus cabal
22	179.5	36.9	100	6	Q9TTQ4	Q9ttq4 equus cabal
23	178	36.6	92	6	Q8MI76	Q8mi76 bos taurus
24	174.5	35.9	99	6	Q8MKC8	Q8mkc8 equus cabal
25	170.5	35.1	97	6	Q8MIT7	Q8mit7 macaca mula
26	168.5	34.7	99	6	Q8HYQ0	Q8hyq0 macaca mula
27	166.5	34.3	100	6	Q95MD5	Q95md5 bos taurus
28	165.5	34.1	97	6	Q8HX25	Q8hxx25 macaca mula
29	164	33.7	50	6	Q8HYN5	Q8hyn5 macaca mula
30	162.5	33.4	81	6	Q9TTQ2	Q9ttq2 equus cabal
31	160	32.9	97	6	Q9TTQ6	Q9ttq6 bos taurus
32	157.5	32.4	95	12	Q98158	Q98158 kaposi's sa
33	157.5	32.4	119	11	Q8K477	Q8k477 rattus norv
34	153	31.5	75	6	Q9TTQ1	Q9ttq1 equus cabal
35	150.5	31.0	91	13	Q8JIM5	Q8jim5 paralichthy
36	150.5	31.0	91	13	Q8AV56	Q8av56 paralichthy
37	149.5	30.8	91	13	Q8JIM4	Q8jim4 paralichthy
38	145	29.8	131	6	Q8HYP5	Q8hyp5 macaca mula
39	137.5	28.3	92	11	Q9QZU2	Q9qzu2 mus musculu
40	137.5	28.3	92	11	Q91ZH5	Q91zh5 rattus norv
41	136.5	28.1	101	12	Q8JRS7	Q8jrs7 guinea pig
42	136	28.0	120	6	Q8HYP4	Q8hyp4 macaca mula
43	135.5	27.9	81	11	Q9QZU1	Q9qzu1 rattus norv
44	135	27.8	95	13	Q8AYB2	Q8ayb2 ictalurus p
45	133.5	27.5	97	11	Q9Z318	Q9z318 cavia porce

ALIGNMENTS

RESULT 1

Q8NHW4	Q8NHW4	PRELIMINARY;	PRT;	92 AA.
AC	Q8NHW4;			
DT	01-OCT-2002 (Tremblrel. 22, Created)			
DT	01-OCT-2002 (Tremblrel. 22, Last sequence update)			
DT	01-MAR-2003 (Tremblrel. 23, Last annotation update)			
DE	Macrophage inflammatory protein-1b2.			
GN	CCL4L1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Nibbs R.J., Barcellos L.F., Townson J.R.;			
RT	"Variation in gene copy number of the human chemokines macrophage			
RT	inflammatory protein-1a/CCL3 and macrophage inflammatory protein-			
RT	1b/CCL4."			
RL	Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.			
DR	EMBL; AY079147; AAL87008.1; -.			
DR	InterPro; IPR000827; CC_chemkine_sml.			
DR	InterPro; IPR001811; Chemokine_IL8.			
DR	Pfam; PF00048; IL8; 1.			
DR	SMART; SM00199; SCY; 1.			
DR	PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.			
SQ	SEQUENCE 92 AA; 10166 MW; 4C8D01E926CDE882 CRC64;			

Query Match 96.3%; Score 468; DB 4; Length 92;  
Best Local Similarity 96.7%; Pred. No. 1.8e-49;  
Matches 89; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY	1	MKLCVTVLSLLMLVAAPFCSPALSPMGSDPPTACCFSTARKLPNFFVVDYETSSLSQ	60
Db	1	MKLCVTVLSLLMLVAAPFCSLALSPMGSDPPTACCFSTARKLPNFFVVDYETSSLSQ	60
QY	61	PAVVFQTKRSKQVCADPSESWMQYVYDLELN	92
Db	61	PAVVFQTKRGKQVCADPSESWMQYVYDLELN	92



QY 61 PAVVFQTKRSKQVCAADPSESWSVQYVVDLELN 92  
 DB 61 PAVVFLTRKGEKVCADPSPQWVNEVVDLELN 92

RESULT 4  
 Q8SQA6 PRELIMINARY; PRT; 93 AA.  
 ID Q8SQA6  
 AC Q8SQA6; (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Macrophage inflammatory protein-1 alpha.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OC NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Werling D.;  
 RT "Role of chemokines in RSV infection."  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY077840; AAL78060.1; -  
 DR InterPro; IPR000827; CC\_chemkine\_sml.  
 DR InterPro; IPR001811; Chemokine\_IL8.  
 DR Pfam; PF00048; IL8; 1.  
 DR SMART; SM00199; SCY; 1.  
 DR PROSITE; PS00472; SMALL CYTOKINES CC; 1.  
 SQ SEQUENCE 93 AA; 10118 MW; 1266BFBFCEE5E8E9 CRC64;

Query Match 65.8%; Score 320; DB 6; Length 93;  
 Best Local Similarity 60.9%; Pred. No. 2.2e-31;  
 Matches 56; Conservative 14; Mismatches 22; Indels 0; Gaps 0;

QY 1 MKLCVTVLSLLMLVAFCSPALSPMGSDPPTACCFSTARKLPNRFVVDYETSSLCQ 60  
 DB 1 MKVAVAAALAVLLCAMALCSQVFSAPFGADTPTACCFSTARKLPNRFVVDYETSSLCQ 60

QY 61 PAVVFQTKRSKQVCAADPSESWSVQYVVDLELN 92  
 DB 61 PGVIFQTKGRQVCANPTEDWVQYITDLELN 92

RESULT 5  
 Q91Z65 PRELIMINARY; PRT; 92 AA.  
 ID Q91Z65  
 AC Q91Z65;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Macrophage inflammatory protein-1 alpha.  
 GN MIP1 ALPHA.  
 OS Sigmodon hispidus (Hispid cotton rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;  
 OC Sigmodon.  
 OC NCBI\_TaxID=42415;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Blanco J.C.; Pletneva L.M.; Prince G.A.;  
 RT "Sigmodon hispidus cytokines, chemokines and interferons."  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF421392; AAL16933.1; -  
 DR HSSP; Q9Y258; IG2S.  
 DR InterPro; IPR000827; CC\_chemkine\_sml.  
 DR InterPro; IPR001811; Chemokine\_IL8.  
 DR Pfam; PF00048; IL8; 1.  
 DR SMART; SM00199; SCY; 1.  
 DR PROSITE; PS00472; SMALL CYTOKINES CC; 1.  
 SQ SEQUENCE 92 AA; 10195 MW; A34FDE21E6FA9C2E CRC64;

Query Match 77.4%; Score 376; DB 11; Length 92;  
 Best Local Similarity 71.7%; Pred. No. 3.1e-38;  
 Matches 66; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

QY 1 MKLCVTVLSLLMLVAFCSPALSPMGSDPPTACCFSTARKLPNRFVVDYETSSLCQ 60  
 DB 1 MKLCSTLALLLLAELFAPVTSAPRGSDPPTISCCFSTARKLPNRFVVDYETSSLCQ 60

[illegible]

Db	2	LAVLLCTMALCN-QFSASLAADTPTACCFYSYTSRQIPQNFMDYFETSSQCKPSVFLT	60
Qy	68	KRSKQVCADPSESVMQEVV	86
Dh	61	KRGROVCADPSEEWQKVV	79

```

RN
RP SEQUENCE FROM N.A.
RA Hughes S.M., Bumstead N.;
RT "Mapping of the gene encoding the chicken homologue of the mammalian
RT chemokine SCYA4.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF146730; AAD48772.1; -.
DR HSSP; P12236; 1HUM.
DR InterPro; IPR000827; CC_chemokine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
SO SEQUENCE 90 AA; 9986 MW; 50AF9679A26751CB CRC64;

```

```

SQ SEQUENCE 90 AA; 9986 MW; 50AF9679A26751CB CRC64;

Query Match      54.3%; Score 264; DB 13; Length 90;
Best Local Similarity 51.1%; Pred. No. 1.5e-24;
Matches 45; Conservative 20; Mismatches 23; Indels 0; Gaps 0

Qy 5 VTVLSLLMLVA AFCSPALSAPMGSDPPTACCFSTYARKLPRNFVVDDYYETSSLCSPAVV 64
   ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:|||||
Db 3 VSVAAALAVLLIAICYQTSAAPVGSDPPTSCCFTYISRQLPFVFADYYETNSQC PHAGVV 62
   ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:|||||

Qy 65 FQTKRSKQVCADPSWSWQEYVYDLELN 92
   ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:|||||
Db 63 FITRKGREVCANQNNDWVQDYNNKMELN 90
   ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:|||||

RESULT 9
Q8HYN3
ID Q8HYN3 PRELIMINARY; PRT; 49 AA.
AC Q8HYN3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Macrophage inflammatory protein 1 beta (Fragment).
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;

```

```
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Hofmann-Lehmann R., Williams A.L., Swenerton R.K., Li P.-L.,
RA Rasmussen R.A., Chenine A.-L., McClure H.M., Ruprecht R.M.;
RT "Quantification of Simian Cytokine and Beta-Chemokine mRNAs using
RT Real-Time Reverse-Transcriptase Polymerase Chain Reaction: Variations
RT in Expression during Chronic Primate Lentivirus Infection.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF457196; AAN76986.1; -.
DR NON_TER 1
FT NON_TER 49
SQ SEQUENCE 49 AA; 5663 MW; D205B56BF349A6CA CRC64;

Query Match 51.9%; Score 252; DB 6; Length 49;
Best Local Similarity 93.9%; Pred. No. 2.2e-23;
Matches 46; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 35 CFSYTARKLPNRFVVDYYETSSLCSPAVVFQTKRSKQVCADPSESWSVQ 83
Db 1 CFSYTVRKLPNRFVVDYYETSSLCSPAVVFQTKRGKQVCADPSETWVQ 49

RESULT 10
Q8HYN4 PRELIMINARY; PRT; 56 AA.
AC Q8HYN4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Macrophage inflammatory protein 1 alpha (Fragment).
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Hofmann-Lehmann R., Williams A.L., Swenerton R.K., Li P.-L.,
RA Rasmussen R.A., Chenine A.-L., McClure H.M., Ruprecht R.M.;
RT "Quantification of Simian Cytokine and Beta-Chemokine mRNAs using
RT Real-Time Reverse-Transcriptase Polymerase Chain Reaction: Variations
RT in Expression during Chronic Primate Lentivirus Infection.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF457195; AAN76985.1; -.
DR NON_TER 1
FT NON_TER 56
SQ SEQUENCE 56 AA; 6442 MW; EB12A0E0D41D6F68 CRC64;

Query Match 51.2%; Score 249; DB 6; Length 56;
Best Local Similarity 73.2%; Pred. No. 6e-23;
Matches 41; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

QY 31 PTACCFSYTARKLPNRFVVDYYETSSLCSPAVVFQTKRSKQVCADPSESWSVQ 86
Db 1 PTACCFSYTSRQIPQNFADYFETSSQCSKPGVILTKRSRQVCADPSEWVKYV 56

RESULT 11
Q9I8E0 PRELIMINARY; PRT; 89 AA.
AC Q9I8E0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Chemokine K203 precursor.
GN K203.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
```

```
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=20170941; PubMed=10704244;
RA Sick C., Schneider K., Staeheli P., Weining K.C.;
RT "Novel chicken CXC and CC chemokines.";
RL Cytokine 12:181-186(2000).
DR EMBL; Y18692; CAB70956.1; -.
DR HSSP; P13236; IHUM.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
KW Signal.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 89 CHEMOKINE K203.
SQ SEQUENCE 89 AA; 9896 MW; 6FA2EA7A4950CA75 CRC64;

Query Match 50.5%; Score 245.5; DB 13; Length 89;
Best Local Similarity 50.0%; Pred. No. 2.6e-22;
Matches 45; Conservative 20; Mismatches 22; Indels 3; Gaps 2;

QY 1 MKLCVTVLSLLMLVAAFCSFALSAPMGSDPPTACCFSYTARKLPNRFVVDYYETSSLC 60
Db 1 MKLSAVVLAL--LIASFCSRASSAPVGPDPVT-CCTTYITHKIPRNLIQRHYSTSTCSK 57

QY 61 PAVVFQTKRSKQVCADPSESWSVQYVVDLE 90
Db 58 PAIIFITKREVCANPSDPVWVQYLSQSVK 87

RESULT 12
Q8MKD0 PRELIMINARY; PRT; 91 AA.
AC Q8MKD0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Small inducible cytokine A5 RANTES.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Takafuji V.A., Sharova L.V., Crisman M.V., Howard R.D.;
RT "Equus caballus RANTES mRNA.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF506970; AAM34212.1; -.
DR InterPro; IPR000827; CC_chemokine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES CC; 1.
SQ SEQUENCE 91 AA; 10159 MW; ABB253E8CD4ED7FD CRC64;

Query Match 50.1%; Score 243.5; DB 6; Length 91;
Best Local Similarity 46.7%; Pred. No. 4.7e-22;
Matches 43; Conservative 22; Mismatches 26; Indels 1; Gaps 1;

QY 1 MKLCVTVLSLLMLVAAFCSFALSAPMGSDPPTACCFSYTARKLPNRFVVDYYETSSLC 60
Db 1 MKVFAAALAVILATATCTCPASAPYASD-TTPCCFAYISRPLPRAHIQYFYTSSKCSI 59

QY 61 PAVVFQTKRSKQVCADPSESWSVQYVVDLELN 92
Db 60 PAVVFVTRKKRQVCANPEKKVREYINTLEMS 91

RESULT 13
Q8HYQ1 PRELIMINARY; PRT; 91 AA.
AC Q8HYQ1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
```





GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 16, 2003, 15:37:55 ; Search time 167.41 Seconds  
(without alignments)  
500.045 Million cell updates/sec

Title: US-09-920-137A-7  
Perfect score: 486  
Sequence: 1 MKLCVTVLSLLMLVAFCSP.....VCADPSESWMQYVYDLELN 92

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 5728757 seqs, 909918778 residues

Total number of hits satisfying chosen parameters: 5728757

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending Patents AA Main:  
1: /cgn2\_6/ptodata/1/paa/PCTUS\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/paa/US06\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/paa/US07\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/paa/US08\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/paa/US081\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/paa/US082\_COMB.pep.\*  
7: /cgn2\_6/ptodata/1/paa/US083\_COMB.pep.\*  
8: /cgn2\_6/ptodata/1/paa/US084\_COMB.pep.\*  
9: /cgn2\_6/ptodata/1/paa/US085\_COMB.pep.\*  
10: /cgn2\_6/ptodata/1/paa/US086\_COMB.pep.\*  
11: /cgn2\_6/ptodata/1/paa/US087\_COMB.pep.\*  
12: /cgn2\_6/ptodata/1/paa/US088\_COMB.pep.\*  
13: /cgn2\_6/ptodata/1/paa/US089\_COMB.pep.\*  
14: /cgn2\_6/ptodata/1/paa/US090\_COMB.pep.\*  
15: /cgn2\_6/ptodata/1/paa/US091\_COMB.pep.\*  
16: /cgn2\_6/ptodata/1/paa/US092\_COMB.pep.\*  
17: /cgn2\_6/ptodata/1/paa/US093\_COMB.pep.\*  
18: /cgn2\_6/ptodata/1/paa/US094\_COMB.pep.\*  
19: /cgn2\_6/ptodata/1/paa/US095\_COMB.pep.\*  
20: /cgn2\_6/ptodata/1/paa/US096\_COMB.pep.\*  
21: /cgn2\_6/ptodata/1/paa/US097A\_COMB.pep.\*  
22: /cgn2\_6/ptodata/1/paa/US097B\_COMB.pep.\*  
23: /cgn2\_6/ptodata/1/paa/US098\_COMB.pep.\*  
24: /cgn2\_6/ptodata/1/paa/US099A\_COMB.pep.\*  
25: /cgn2\_6/ptodata/1/paa/US099B\_COMB.pep.\*  
26: /cgn2\_6/ptodata/1/paa/US100\_COMB.pep.\*  
27: /cgn2\_6/ptodata/1/paa/US101\_COMB.pep.\*  
28: /cgn2\_6/ptodata/1/paa/US102\_COMB.pep.\*  
29: /cgn2\_6/ptodata/1/paa/US103\_COMB.pep.\*  
30: /cgn2\_6/ptodata/1/paa/US104\_COMB.pep.\*  
31: /cgn2\_6/ptodata/1/paa/US106\_COMB.pep.\*  
32: /cgn2\_6/ptodata/1/paa/US60\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	486	100.0	92	1	PCT-US94-08207A-28
					Sequence 28, Appl

2	486	100.0	92	1	PCT-US94-08207-28	Sequence 28, Appl
3	486	100.0	92	1	PCT-US97-17900-10	Sequence 10, Appl
4	486	100.0	92	1	PCT-US98-04002-10	Sequence 10, Appl
5	486	100.0	92	5	US-08-136-117-28	Sequence 28, Appl
6	486	100.0	92	7	US-08-390-7408-7	Sequence 7, Appl
7	486	100.0	92	8	US-08-467-123-4	Sequence 4, Appl
8	486	100.0	92	13	US-08-927-939-20	Sequence 20, Appl
9	486	100.0	92	13	US-08-927-939A-20	Sequence 20, Appl
10	486	100.0	92	13	US-08-940-687-10	Sequence 10, Appl
11	486	100.0	92	14	US-09-023-092-8	Sequence 8, Appl
12	486	100.0	92	14	US-09-081-230-3	Sequence 3, Appl
13	486	100.0	92	15	US-09-113-705-4	Sequence 4, Appl
14	486	100.0	92	15	US-09-113-705-7	Sequence 7, Appl
15	486	100.0	92	15	US-09-150-813-20	Sequence 20, Appl
16	486	100.0	92	16	US-09-208-803-11	Sequence 11, Appl
17	486	100.0	92	17	US-09-360-290-7	Sequence 7, Appl
18	486	100.0	92	17	US-09-387-620-4	Sequence 4, Appl
19	486	100.0	92	18	US-09-467-638-10	Sequence 10, Appl
20	486	100.0	92	19	US-09-545-894-10	Sequence 10, Appl
21	486	100.0	92	22	US-09-791-537-22748	Sequence 22748, A
22	486	100.0	92	23	US-09-834-366-17997	Sequence 17997, A
23	486	100.0	92	23	US-09-834-794A-31	Sequence 31, Appl
24	486	100.0	92	23	US-09-834-795A-31	Sequence 31, Appl
25	486	100.0	92	24	US-09-920-137A-7	Sequence 7, Appl
26	486	100.0	92	26	US-10-057-275-7	Sequence 7, Appl
27	486	100.0	92	27	US-10-137-655-7	Sequence 7, Appl
28	486	100.0	92	27	US-10-158-366-4	Sequence 4, Appl
29	486	100.0	92	28	US-10-293-705-11	Sequence 11, Appl
30	486	100.0	92	29	US-10-325-899-9374	Sequence 9374, Ap
31	486	100.0	92	30	US-10-405-027-4023	Sequence 4023, Ap
32	486	100.0	92	32	US-60-197-873-17997	Sequence 17997, A
33	486	100.0	92	32	US-60-453-050-9427	Sequence 9427, Ap
34	486	100.0	92	32	US-60-453-135-9427	Sequence 9427, Ap
35	486	100.0	92	32	US-60-455-444-5106	Sequence 5106, Ap
36	486	100.0	92	32	US-60-465-241-5106	Sequence 5106, Ap
37	486	100.0	92	32	US-60-466-412-9427	Sequence 9427, Ap
38	486	100.0	92	32	US-60-474-850-516	Sequence 516, App
39	486	100.0	331	1	PCT-US98-04002-7	Sequence 7, Appl
40	486	100.0	331	18	US-09-467-638-7	Sequence 7, Appl
41	483	99.4	92	27	US-10-170-385-407	Sequence 407, App
42	482	99.2	92	21	US-09-724-676-63090	Sequence 63090, A
43	482	99.2	92	21	US-09-724-676-63091	Sequence 63091, A
44	482	99.2	92	21	US-09-724-676-63101	Sequence 63101, A
45	482	99.2	92	21	US-09-724-676-63102	Sequence 63102, A

ALIGNMENTS

RESULT 1  
PCT-US94-08207A-28  
; Sequence 28, Application PC/TUS9408207A  
; GENERAL INFORMATION:  
; APPLICANT: The Upjohn Company  
; TITLE OF INVENTION: FOR U.S. PURPOSES ONLY: Hoogewerf, Arlene J. and Ledbetter, Steven R.  
; TITLE OF INVENTION: USE OF HEPARANASE TO IDENTIFY AND  
; TITLE OF INVENTION: ISOLATE ANTI-HEPARANASE COMPOUNDS  
; NUMBER OF SEQUENCES: 43  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: The Upjohn Company, Intellectual Property Law  
; STREET: 301 Henrietta  
; CITY: Kalamazoo  
; STATE: MI  
; COUNTRY: USA  
; ZIP: 49001  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/08207A  
; FILING DATE:



APPLICANT: Herrmann, Steve  
APPLICANT: Swanberg, Stephen  
TITLE OF INVENTION: CHIMERIC POLYPEPTIDES CONTAINING  
TITLE OF INVENTION: CHEMOKINE DOMAINS  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genetics Institute, Inc.  
STREET: 87 CambridgePark  
CITY: Cambridge  
STATE: MA  
COUNTRY: USA  
ZIP: 02140  
COMPUTER READABLE FORM: Floppy disk  
MEDIUM TYPE: IBM PC compatible  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US98/04002  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Sprunger, Suzanne  
REGISTRATION NUMBER: P-41,323  
REFERENCE/DOCKET NUMBER: GI5291  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 498-8284  
TELEFAX: (617) 876-5851  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 92 amino acids  
TYPE: amino acid  
STRANDEDNESS: linear  
MOLECULE TYPE: protein  
PCT-US98-04002-10

Query Match 100.0%; Score 486; DB 1; Length 92;  
Best Local Similarity 100.0%; Pred. No. 5.1e-48;  
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLCVTVLSLLMLVAFCSPALSPMGSDPPTACCFSTYARKLPNFVVDYYETSSLCSQ 60  
|||||  
Db 1 MKLCVTVLSLLMLVAFCSPALSPMGSDPPTACCFSTYARKLPNFVVDYYETSSLCSQ 60  
QY 61 PAVVFQTKRSKQVCADPSESWSVQYVYDLELN 92  
|||||  
Db 61 PAVVFQTKRSKQVCADPSESWSVQYVYDLELN 92

RESULT 5  
US-08-136-117-28  
Sequence 28, Application US/08136117  
GENERAL INFORMATION:  
APPLICANT: Hoogewerf, Arlene J.  
APPLICANT: Ledbetter, Steven R.  
TITLE OF INVENTION: USE OF HEPARANASE TO IDENTIFY AND  
TITLE OF INVENTION: ISOLATE ANTI-HEPARANASE COMPOUNDS  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: The Upjohn Company, Intellectual Property Law  
STREET: 301 Henrietta  
CITY: Kalamazoo  
STATE: MI  
COUNTRY: USA  
ZIP: 49001  
COMPUTER READABLE FORM: Floppy disk  
MEDIUM TYPE: IBM PC compatible  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/136,117

FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Jameson, William G.  
REGISTRATION NUMBER: 27,199  
REFERENCE/DOCKET NUMBER: 4731.1 CP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 616/385-7561  
TELEFAX: 616/385-6897  
TELEX: 224401  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 92 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-136-117-28

Query Match 100.0%; Score 486; DB 5; Length 92;  
Best Local Similarity 100.0%; Pred. No. 5.1e-48;  
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLCVTVLSLLMLVAFCSPALSPMGSDPPTACCFSTYARKLPNFVVDYYETSSLCSQ 60  
|||||  
Db 1 MKLCVTVLSLLMLVAFCSPALSPMGSDPPTACCFSTYARKLPNFVVDYYETSSLCSQ 60  
QY 61 PAVVFQTKRSKQVCADPSESWSVQYVYDLELN 92  
|||||  
Db 61 PAVVFQTKRSKQVCADPSESWSVQYVYDLELN 92

RESULT 6  
US-08-390-740B-7  
Sequence 7, Application US/08390740B  
GENERAL INFORMATION:  
APPLICANT: Coleman, Roger  
APPLICANT: Bandman, Olga  
APPLICANT: Wilde, Craig G.  
TITLE OF INVENTION: NEW CHEMOKINES EXPRESSED IN PANCREAS  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/390,740B  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Luther, Barbara J.  
REGISTRATION NUMBER: 33,954  
REFERENCE/DOCKET NUMBER: PF-0027 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-852-0195  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 92 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: MIP-1b

US-08-390-740B-7

Query Match 100.0%; Score 486; DB 7; Length 92;  
Best Local Similarity 100.0%; Pred. NO. 5.1e-48;  
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLCVTVLSLLMLVAFCSPALSPALSGDPPTACCFSTARKLPNRFVVDYVYETSSLC SQ 60  
Db 1 MKLCVTVLSLLMLVAFCSPALSPALSGDPPTACCFSTARKLPNRFVVDYVYETSSLC SQ 60

QY 61 PAVVFQTKRSKQVCADPSESWSVQYVYDLELN 92  
Db 61 PAVVFQTKRSKQVCADPSESWSVQYVYDLELN 92

## RESULT 7

US-08-467-123-4  
; Sequence 4, Application US/08467123  
; GENERAL INFORMATION:  
; APPLICANT: Coleman, Roger  
; APPLICANT: Wilde, Craig G.  
; APPLICANT: Seilhamer, Jeffrey J.  
; TITLE OF INVENTION: A NEW CHEMOKINE EXPRESSED IN FETAL SPLEEN,  
; TITLE OF INVENTION: ITS PRODUCTION AND USES

; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3330 HILLVIEW AVENUE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/467,123  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/375,346  
; FILING DATE: 19-JAN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: LUTHER, BARBARA J.  
; REGISTRATION NUMBER: 33,954  
; REFERENCE/DOCKET NUMBER: PF-0026 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 855-0555  
; TELEFAX: (415) 855-0572  
; TELEX:

; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 92 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
; ORIGINAL SOURCE:  
US-08-467-123-4

Query Match 100.0%; Score 486; DB 8; Length 92;  
Best Local Similarity 100.0%; Pred. NO. 5.1e-48;  
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLCVTVLSLLMLVAFCSPALSPALSGDPPTACCFSTARKLPNRFVVDYVYETSSLC SQ 60  
Db 1 MKLCVTVLSLLMLVAFCSPALSPALSGDPPTACCFSTARKLPNRFVVDYVYETSSLC SQ 60

QY 61 PAVVFQTKRSKQVCADPSESWSVQYVYDLELN 92  
Db 61 PAVVFQTKRSKQVCADPSESWSVQYVYDLELN 92

## RESULT 8

US-08-927-939-20  
; Sequence 20, Application US/08927939  
; GENERAL INFORMATION:  
; APPLICANT: Grainger, David J.  
; APPLICANT: Tatalick, Lauren Marie  
; TITLE OF INVENTION: Compounds and methods to inhibit or  
; TITLE OF INVENTION: augment an inflammatory response.

; FILE REFERENCE: 295.022US1  
; CURRENT APPLICATION NUMBER: US/08/927,939  
; CURRENT FILING DATE: 1997-09-11  
; NUMBER OF SEQ ID NOS: 83  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 20  
; LENGTH: 92  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-08-927-939-20

Query Match 100.0%; Score 486; DB 13; Length 92;  
Best Local Similarity 100.0%; Pred. NO. 5.1e-48;  
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLCVTVLSLLMLVAFCSPALSPALSGDPPTACCFSTARKLPNRFVVDYVYETSSLC SQ 60  
Db 1 MKLCVTVLSLLMLVAFCSPALSPALSGDPPTACCFSTARKLPNRFVVDYVYETSSLC SQ 60

QY 61 PAVVFQTKRSKQVCADPSESWSVQYVYDLELN 92  
Db 61 PAVVFQTKRSKQVCADPSESWSVQYVYDLELN 92

## RESULT 9

US-08-927-939A-20  
; Sequence 20, Application US/08927939A  
; GENERAL INFORMATION:  
; APPLICANT: Grainger, David J.  
; APPLICANT: Tatalick, Lauren Marie  
; TITLE OF INVENTION: Compounds and methods to inhibit or  
; TITLE OF INVENTION: augment an inflammatory response.

; FILE REFERENCE: 1543.001US1  
; CURRENT APPLICATION NUMBER: US/08/927,939A  
; CURRENT FILING DATE: 1997-11-09  
; NUMBER OF SEQ ID NOS: 85  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 20  
; LENGTH: 92  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-08-927-939A-20

Query Match 100.0%; Score 486; DB 13; Length 92;  
Best Local Similarity 100.0%; Pred. NO. 5.1e-48;  
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLCVTVLSLLMLVAFCSPALSPALSGDPPTACCFSTARKLPNRFVVDYVYETSSLC SQ 60  
Db 1 MKLCVTVLSLLMLVAFCSPALSPALSGDPPTACCFSTARKLPNRFVVDYVYETSSLC SQ 60

QY 61 PAVVFQTKRSKQVCADPSESWSVQYVYDLELN 92  
Db 61 PAVVFQTKRSKQVCADPSESWSVQYVYDLELN 92

## RESULT 10

US-08-940-687-10  
; Sequence 10, Application US/08940687  
; GENERAL INFORMATION:



APPLICANT: Luster, Andrew D.  
APPLICANT: Garcia-zepeda, Eduardo A.  
APPLICANT: Sarafi, Mindy N.  
TITLE OF INVENTION: MCP-4 AND MCP-5: NOVEL CHEMOKINES  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Clark & Elbing LLP  
STREET: 176 Federal Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/940,687  
FILING DATE:  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/027,128  
FILING DATE: 30-SEP-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Bieker-Brady, Kristina  
REGISTRATION NUMBER: 39,109  
REFERENCE/DOCKET NUMBER: 00786/293002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-428-0200  
TELEFAX: 617-428-7045  
TELEX:  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 92 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-940-687-10

Query Match 100.0%; Score 486; DB 13; Length 92;  
Best Local Similarity 100.0%; Pred. No. 5.le-48;  
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLCVTVLSLLMLVAFCSPALSGSDPPTACCFSTARKLPNRFVVDYYETSSLSQ 60  
|||||  
Db 1 MKLCVTVLSLLMLVAFCSPALSGSDPPTACCFSTARKLPNRFVVDYYETSSLSQ 60

QY 61 PAVVFQTKRSKQVCADPSESWSVQEVYVDLELN 92  
|||||  
Db 61 PAVVFQTKRSKQVCADPSESWSVQEVYVDLELN 92

RESULT 11

US-09-023-092-8  
Sequence 8, Application US/09023092  
GENERAL INFORMATION:  
APPLICANT: Hedrick, Joseph A.  
APPLICANT: Wang, Luquan  
APPLICANT: Zlotnik, Albert  
APPLICANT: Murgolo, Nicholas J.  
APPLICANT: Greene, Jonathan R.  
TITLE OF INVENTION: Mammalian Chemokines; Related Reagents  
TITLE OF INVENTION: and Methods  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DNAX Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/023,092  
FILING DATE: 13-FEB-1998  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0780  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650)852-9196  
TELEFAX: (650)496-1200  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 92 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-09-023-092-8

Query Match 100.0%; Score 486; DB 14; Length 92;  
Best Local Similarity 100.0%; Pred. No. 5.le-48;  
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLCVTVLSLLMLVAFCSPALSGSDPPTACCFSTARKLPNRFVVDYYETSSLSQ 60  
|||||  
Db 1 MKLCVTVLSLLMLVAFCSPALSGSDPPTACCFSTARKLPNRFVVDYYETSSLSQ 60

QY 61 PAVVFQTKRSKQVCADPSESWSVQEVYVDLELN 92  
|||||  
Db 61 PAVVFQTKRSKQVCADPSESWSVQEVYVDLELN 92

RESULT 12

US-09-081-230-3  
Sequence 3, Application US/09081230  
GENERAL INFORMATION:  
APPLICANT: Sheppard, Paul  
TITLE OF INVENTION: HUMAN CHEMOKINE ZCHEMO-8  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ZymoGenetics  
STREET: 1201 Eastlake Ave. E.  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98102  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/081,230  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Lingenfelter, Susan E  
REGISTRATION NUMBER: 41,156  
REFERENCE/DOCKET NUMBER: 97-23  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-442-6675  
TELEFAX: 206-442-6678  
TELEX:  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:



Search completed: December 16, 2003, 15:46:43  
Job time : 168.41 secs

---

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 16, 2003, 15:38:25 ; Search time 13.5738 Seconds  
(without alignments)  
366.280 Million cell updates/sec

Title: US-09-920-137A-7  
Perfect score: 486  
Sequence: 1 MKLCVTVLSLLMLVAFCSP.....VCADPSESWMQYVYDLELN 92

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 285895 seqs, 54041359 residues

Total number of hits satisfying chosen parameters: 285895

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending Patents\_AA\_New:\*  
1: /cgn2\_6/ptodata/2/paa/PCT\_NEW\_COMB.pep:\*  
2: /cgn2\_6/ptodata/2/paa/US06\_NEW\_COMB.pep:\*  
3: /cgn2\_6/ptodata/2/paa/US07\_NEW\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/paa/US08\_NEW\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/paa/US09\_NEW\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/paa/US10\_NEW\_COMB.pep:\*  
7: /cgn2\_6/ptodata/2/paa/US60\_NEW\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	486	100.0	92	US-60-487-610-1666	Sequence 1666, Ap
2	486	100.0	92	US-60-487-610-1677	Sequence 1677, Ap
3	486	100.0	92	US-60-485-450-1051	Sequence 1051, Ap
4	486	100.0	92	US-60-485-450-1057	Sequence 1057, Ap
5	375	77.2	69	US-10-332-038A-9	Sequence 9, Appli
6	371	76.3	68	US-10-622-134-10	Sequence 10, Appl
7	359	73.9	72	US-60-487-610-1667	Sequence 1667, Ap
8	359	73.9	72	US-60-485-450-1052	Sequence 1052, Ap
9	357	73.5	69	US-10-398-457-5	Sequence 5, Appli
10	300.5	61.8	92	PCT-US03-21703-42	Sequence 42, Appl
11	296.5	61.0	92	US-60-487-610-1678	Sequence 1678, Ap
12	296.5	61.0	92	US-60-485-450-1058	Sequence 1058, Ap
13	278	57.2	70	US-10-332-038A-8	Sequence 8, Appli
14	278	57.2	70	US-10-398-457-31	Sequence 31, Appl
15	275	56.6	69	PCT-US03-28745-3	Sequence 3, Appli
16	275	56.6	69	US-10-622-134-9	Sequence 9, Appli
17	263	54.1	70	US-10-398-457-4	Sequence 4, Appli
18	246.5	50.7	91	US-10-398-457-12	Sequence 12, Appl
19	245.5	50.5	91	US-10-398-457-1	Sequence 1, Appli
20	245.5	50.5	91	US-60-487-610-2474	Sequence 2474, Ap
21	245.5	50.5	91	US-60-485-450-1561	Sequence 1561, Ap
22	243.5	50.1	91	US-10-398-457-11	Sequence 11, Appl
23	243.5	50.1	91	US-10-398-457-13	Sequence 13, Appl
24	242.5	49.9	91	US-10-398-457-6	Sequence 6, Appli
25	242.5	49.9	91	US-10-398-457-8	Sequence 8, Appli
26	242.5	49.9	91	US-10-398-457-9	Sequence 9, Appli

27	242.5	49.9	91	6	US-10-398-457-10	Sequence 10, Appl
28	236.5	48.7	91	6	US-10-398-457-3	Sequence 3, Appli
29	226	46.5	92	6	US-10-398-457-7	Sequence 7, Appli
30	224.5	46.2	93	6	US-10-474-794-277	Sequence 277, App
31	224.5	46.2	93	6	US-10-474-794-279	Sequence 279, App
32	224.5	46.2	93	6	US-10-474-794-281	Sequence 281, App
33	224.5	46.2	93	7	US-60-487-610-2476	Sequence 2476, Ap
34	212	43.6	74	6	US-10-332-038A-15	Sequence 15, Appl
35	212	43.6	74	6	US-10-398-457-35	Sequence 35, Appl
36	210	43.2	89	7	US-60-487-610-2330	Sequence 2330, Ap
37	199.5	41.0	68	1	PCT-US03-28745-4	Sequence 4, Appli
38	199.5	41.0	68	6	US-10-622-134-11	Sequence 11, Appl
39	199.5	41.0	68	6	US-10-332-038A-2	Sequence 2, Appli
40	199	40.9	98	6	US-10-646-770-4	Sequence 4, Appli
41	199	40.9	98	7	US-60-487-610-2399	Sequence 2399, Ap
42	196	40.3	69	6	US-10-658-733-21	Sequence 21, Appl
43	192.5	39.6	99	1	PCT-US03-21703-41	Sequence 41, Appl
44	192.5	39.6	99	6	US-10-646-770-18	Sequence 18, Appl
45	187	38.5	66	6	US-10-398-457-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1  
US-60-487-610-1666  
; Sequence 1666, Application US/60487610  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele  
; APPLICANT: HUANG, Hongjin  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,  
; TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001469  
; CURRENT APPLICATION NUMBER: US/60/487,610  
; CURRENT FILING DATE: 2003-07-17  
; NUMBER OF SEQ ID NOS: 97101  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1666  
; LENGTH: 92  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-60-487-610-1666

Query Match 100.0%; Score 486; DB 7; Length 92;  
Best Local Similarity 100.0%; Pred. No. 3.3e-50;  
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLCVTVLSLLMLVAFCSPALSGMDPPTACCFSTARKLPNRFVVDYETSLCSQ 60  
Db 1 MKLCVTVLSLLMLVAFCSPALSGMDPPTACCFSTARKLPNRFVVDYETSLCSQ 60

QY 61 PAVVFQTKRSKQVCADPSESWMQYVYDLELN 92  
Db 61 PAVVFQTKRSKQVCADPSESWMQYVYDLELN 92

RESULT 2  
US-60-487-610-1677  
; Sequence 1677, Application US/60487610  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele  
; APPLICANT: HUANG, Hongjin  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,  
; TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001469  
; CURRENT APPLICATION NUMBER: US/60/487,610  
; CURRENT FILING DATE: 2003-07-17  
; NUMBER OF SEQ ID NOS: 97101  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1677  
; LENGTH: 92



```

; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-487-610-1677

Query Match
Best Local Similarity 100.0%; Score 486; DB 7; Length 92;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLCVTVLSLLMLVAFCSPALSPALSGDPPPTACCFSTYARKLPRNFVVDYYETSSLC SQ 60
Db 1 MKLCVTVLSLLMLVAFCSPALSPALSGDPPPTACCFSTYARKLPRNFVVDYYETSSLC SQ 60

QY 61 PAVVFQTKRSKQVCADPSESWSVQYVYDLELN 92
Db 61 PAVVFQTKRSKQVCADPSESWSVQYVYDLELN 92

RESULT 3
US-60-485-450-1051
; Sequence 1051, Application US/60485450
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: CHANG, Sheng-Yung
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C
; TITLE OF INVENTION: VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001470
; CURRENT APPLICATION NUMBER: US/60/485,450
; CURRENT FILING DATE: 2003-07-09
; NUMBER OF SEQ ID NOS: 47859
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1051
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-485-450-1051

Query Match
Best Local Similarity 100.0%; Score 486; DB 7; Length 92;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLCVTVLSLLMLVAFCSPALSPALSGDPPPTACCFSTYARKLPRNFVVDYYETSSLC SQ 60
Db 1 MKLCVTVLSLLMLVAFCSPALSPALSGDPPPTACCFSTYARKLPRNFVVDYYETSSLC SQ 60

QY 61 PAVVFQTKRSKQVCADPSESWSVQYVYDLELN 92
Db 61 PAVVFQTKRSKQVCADPSESWSVQYVYDLELN 92

RESULT 4
US-60-485-450-1057
; Sequence 1057, Application US/60485450
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: CHANG, Sheng-Yung
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C
; TITLE OF INVENTION: VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001470
; CURRENT APPLICATION NUMBER: US/60/485,450
; CURRENT FILING DATE: 2003-07-09
; NUMBER OF SEQ ID NOS: 47859
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1057
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-485-450-1057

Query Match
100.0%; Score 486; DB 7; Length 92;
```

```

Best Local Similarity 100.0%; Pred. No. 3.3e-50;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLCVTVLSLLMLVAFCSPALSPALSGDPPPTACCFSTYARKLPRNFVVDYYETSSLC SQ 60
Db 1 MKLCVTVLSLLMLVAFCSPALSPALSGDPPPTACCFSTYARKLPRNFVVDYYETSSLC SQ 60

QY 61 PAVVFQTKRSKQVCADPSESWSVQYVYDLELN 92
Db 61 PAVVFQTKRSKQVCADPSESWSVQYVYDLELN 92

RESULT 5
US-10-332-038A-9
; Sequence 9, Application US/10332038A
; GENERAL INFORMATION:
; APPLICANT: Gryphon Therapeutics, Inc.
; APPLICANT: Offord, Robin
; APPLICANT: Gaertner, Hubert
; APPLICANT: Hartley, Oliver
; TITLE OF INVENTION: Chemokine Receptor Modulators, Production and Use
; FILE REFERENCE: 03504.271
; CURRENT APPLICATION NUMBER: US/10/332,038A
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: US 60/217,683
; PRIOR FILING DATE: 2000-07-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-332-038A-9

Query Match
77.2%; Score 375; DB 6; Length 69;
Best Local Similarity 100.0%; Pred. No. 3e-37;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 APMGSDPPTACCFSTYARKLPRNFVVDYYETSSLC SQPAVVFQTKRSKQVCADPSESWSVQ 83
Db 1 APMGSDPPTACCFSTYARKLPRNFVVDYYETSSLC SQPAVVFQTKRSKQVCADPSESWSVQ 60

QY 84 EYVYDLELN 92
Db 61 EYVYDLELN 69

RESULT 6
US-10-622-134-10
; Sequence 10, Application US/10622134
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, TIMOTHY J.
; JOSE, PETER J.
; GRIFFITHS-JOHNSON, DAVID A.
; HSUAN, JOHN J.
; TITLE OF INVENTION: CHEMOTACTIC CYTOKINE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/622,134
; FILING DATE: 18-Jul-2003
; CLASSIFICATION: 424
```

```
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/291,038
; FILING DATE: 14-Apr-1999
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/08/615,232A
; FILING DATE: 13-AUG-1996
; APPLICATION NUMBER: GB 9318984
; FILING DATE: 14-SEP-1993
; APPLICATION NUMBER: GB 9408602
; FILING DATE: 29-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 550-32
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 68 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-622-134-10
      Query Match      76.3%; Score 371; DB 6; Length 68;
      Best Local Similarity 100.0%; Pred. No. 8.7e-37;
      Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 PMGSDPPTACCFSYTARKLPRNFVVDYETSSLCSPQAVVFQTKRSKQVCADPSESWMQ 84
Db 1 PMGSDPPTACCFSYTARKLPRNFVVDYETSSLCSPQAVVFQTKRSKQVCADPSESWMQ 60

QY 85 YVYDLELN 92
Db 61 YVYDLELN 68

RESULT 7
US-60-487-610-1667
; Sequence 1667, Application US/60487610
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
; TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001469
; CURRENT APPLICATION NUMBER: US/60/487,610
; CURRENT FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 97101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1667
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-487-610-1667
      Query Match      73.9%; Score 359; DB 7; Length 72;
      Best Local Similarity 78.3%; Pred. No. 2.4e-35;
      Matches 72; Conservative 0; Mismatches 0; Indels 20; Gaps 1;

QY 1 MKLCVTVLSLLMLVAAFCSFALSAPMGSDPPTACCFSYTARKLPRNFVVDYETSSLC 60
Db 1 MKLCVTVLSLLMLVAAFCSFALSAPMGSDPPTACCFSYTARKLPRNFVVDYETSSLC 60
QY 61 PAVVFQTKRSKQVCADPSESWMQYVYDLELN 92
Db 61 PAV-----EYVYDLELN 72
```

```
RESULT 8
US-60-485-450-1052
; Sequence 1052, Application US/60485450
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: CHANG, Sheng-Yung
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C
; TITLE OF INVENTION: VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001470
; CURRENT APPLICATION NUMBER: US/60/485,450
; CURRENT FILING DATE: 2003-07-09
; NUMBER OF SEQ ID NOS: 47859
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1052
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-485-450-1052
      Query Match      73.9%; Score 359; DB 7; Length 72;
      Best Local Similarity 78.3%; Pred. No. 2.4e-35;
      Matches 72; Conservative 0; Mismatches 0; Indels 20; Gaps 1;

QY 1 MKLCVTVLSLLMLVAAFCSFALSAPMGSDPPTACCFSYTARKLPRNFVVDYETSSLC 60
Db 1 MKLCVTVLSLLMLVAAFCSFALSAPMGSDPPTACCFSYTARKLPRNFVVDYETSSLC 60
QY 61 PAVVFQTKRSKQVCADPSESWMQYVYDLELN 92
Db 61 PAV-----EYVYDLELN 72

RESULT 9
US-10-398-457-5
; Sequence 5, Application US/10398457
; GENERAL INFORMATION:
; APPLICANT: APPLIED RESEARCH SYSTEMS ARS HOLDING N.V.
; TITLE OF INVENTION: CHEMOKINES MUTANTS IN THE TREATMENT OF MULTIPLE SCLEROSIS
; FILE REFERENCE: WO465
; CURRENT APPLICATION NUMBER: US/10/398,457
; CURRENT FILING DATE: 2003-11-13
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Escherichia Coli
US-10-398-457-5
      Query Match      73.5%; Score 357; DB 6; Length 69;
      Best Local Similarity 95.7%; Pred. No. 4e-35;
      Matches 66; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 24 APMGSDPPTACCFSYTARKLPRNFVVDYETSSLCSPQAVVFQTKRSKQVCADPSESWMQ 83
Db 1 APMGSDPPTACCFSYTARKLPRNFVVDYETSSLCSPQAVVFQTKRSKQVCADPSESWMQ 60
QY 84 EYVYDLELN 92
Db 61 EYVYDLELN 69

RESULT 10
PCT-US03-21703-42
; Sequence 42, Application PC/TUS0321703
; GENERAL INFORMATION:
; APPLICANT: Rupp, Fabio
; APPLICANT: Wang, Jianrui
; APPLICANT: Zhou, Ping
; APPLICANT: Wehrman, Tom
```

APPLICANT: Wang, Zhiwei  
APPLICANT: Tang, Y. Tom  
TITLE OF INVENTION: Methods and Materials Relating to Novel Polypeptides and Polynucle  
FILE REFERENCE: HYS-B2 PCT  
CURRENT APPLICATION NUMBER: PCT/US03/21703  
CURRENT FILING DATE: 2003-07-09  
PRIOR APPLICATION NUMBER: PCT/US02/29636  
PRIOR FILING DATE: 2002-09-18  
PRIOR APPLICATION NUMBER: 60/395,402  
PRIOR FILING DATE: 2002-07-12  
PRIOR APPLICATION NUMBER: PCT/US02/22858  
PRIOR FILING DATE: 2002-07-19  
PRIOR APPLICATION NUMBER: 10/112,944  
PRIOR FILING DATE: 2002-03-28  
PRIOR APPLICATION NUMBER: 60/306,971  
PRIOR FILING DATE: 2001-07-21  
PRIOR APPLICATION NUMBER: 10/296,115  
PRIOR FILING DATE: 2002-11-18  
PRIOR APPLICATION NUMBER: PCT/US00/35017  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: 09/488,725  
PRIOR FILING DATE: 2000-01-21  
PRIOR APPLICATION NUMBER: 60/418,132  
PRIOR FILING DATE: 2002-10-11  
PRIOR APPLICATION NUMBER: PCT/US02/39555  
PRIOR FILING DATE: 2002-12-10  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 110  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 42  
LENGTH: 92  
TYPE: PRT  
ORGANISM: Homo sapiens  
PCT-US03-21703-42

Query Match 61.8%; Score 300.5; DB 1; Length 92;  
Best Local Similarity 57.6%; Pred. No. 2.6e-28;  
Matches 53; Conservative 19; Mismatches 19; Indels 1; Gaps 1;  
QY 1 MKLCVTVLSLLMLVAFCSPALSPMGSDPPTACCFSYTARKLPNRFVVDYYETSSLSQ 60  
Db 1 MQVSTAALAVLLCTMALCN-QFSASLAADTPTACCFSYTSRQIPQNFIAFYFETSSQCSK 59

QY 61 PAVVFQTKRSKQVCADPSESQVYVYDLELN 92  
Db 60 PGVIFLTKRGRQVCADPSEEWQKYVSDLELS 91

RESULT 11  
US-60-487-610-1678  
Sequence 1678, Application US/60487610  
GENERAL INFORMATION:  
APPLICANT: CARGILL, Michele  
APPLICANT: HUANG, Hongjin  
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,  
TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001469  
CURRENT APPLICATION NUMBER: US/60/487,610  
CURRENT FILING DATE: 2003-07-17  
NUMBER OF SEQ ID NOS: 97101  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 1678  
LENGTH: 92  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-60-487-610-1678

Query Match 61.0%; Score 296.5; DB 7; Length 92;  
Best Local Similarity 56.5%; Pred. No. 7.8e-28;  
Matches 52; Conservative 19; Mismatches 20; Indels 1; Gaps 1;  
QY 1 MKLCVTVLSLLMLVAFCSPALSPMGSDPPTACCFSYTARKLPNRFVVDYYETSSLSQ 60

Db 1 MQVSTAALAVLLCTMALCN-QFSASLAADTPTACCFSYTSRQIPQNFIAFYFETSSQCSK 59  
QY 61 PAVVFQTKRSKQVCADPSESQVYVYDLELN 92  
Db 60 PGVIFLTKRGRQVCADPSEEWQKYVSDLELS 91  
RESULT 12  
US-60-485-450-1058  
Sequence 1058, Application US/60485450  
GENERAL INFORMATION:  
APPLICANT: CARGILL, Michele  
APPLICANT: CHANG, Sheng-Yung  
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C  
TITLE OF INVENTION: VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES  
TITLE OF INVENTION: THEREOF  
FILE REFERENCE: CL001470  
CURRENT APPLICATION NUMBER: US/60/485,450  
CURRENT FILING DATE: 2003-07-09  
NUMBER OF SEQ ID NOS: 47859  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 1058  
LENGTH: 92  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-60-485-450-1058

Query Match 61.0%; Score 296.5; DB 7; Length 92;  
Best Local Similarity 56.5%; Pred. No. 7.8e-28;  
Matches 52; Conservative 19; Mismatches 20; Indels 1; Gaps 1;  
QY 1 MKLCVTVLSLLMLVAFCSPALSPMGSDPPTACCFSYTARKLPNRFVVDYYETSSLSQ 60  
Db 1 MQVSTAALAVLLCTMALCN-QFSASLAADTPTACCFSYTSRQIPQNFIAFYFETSSQCSK 59  
QY 61 PAVVFQTKRSKQVCADPSESQVYVYDLELN 92  
Db 60 PGVIFLTKRGRQVCADPSEEWQKYVSDLELS 91

RESULT 13  
US-10-332-038A-8  
Sequence 8, Application US/10332038A  
GENERAL INFORMATION:  
APPLICANT: Gryphon Therapeutics, Inc.  
APPLICANT: Offord, Robin  
APPLICANT: Gaertner, Hubert  
APPLICANT: Hartley, Oliver  
TITLE OF INVENTION: Chemokine Receptor Modulators, Production and Use  
FILE REFERENCE: 03504.271  
CURRENT APPLICATION NUMBER: US/10/332,038A  
CURRENT FILING DATE: 2003-05-06  
PRIOR APPLICATION NUMBER: US 60/217,683  
PRIOR FILING DATE: 2000-07-12  
NUMBER OF SEQ ID NOS: 28  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 8  
LENGTH: 70  
TYPE: PRT  
ORGANISM: Homo Sapiens  
US-10-332-038A-8

Query Match 57.2%; Score 278; DB 6; Length 70;  
Best Local Similarity 68.1%; Pred. No. 8.6e-26;  
Matches 47; Conservative 13; Mismatches 9; Indels 0; Gaps 0;  
QY 24 APMGSDPPTACCFSYTARKLPNRFVVDYYETSSLSQPAVVFQTKRSKQVCADPSESQV 83  
Db 1 ASLAADTPTACCFSYTSRQIPQNFIAFYFETSSQCSKPGVIFLTKRGRQVCADPSEEWQ 60

QY 84 EVVYDLELN 92

Db 61 KYVSDLELS 69

RESULT 14  
US-10-398-457-31  
; Sequence 31, Application US/10398457  
; GENERAL INFORMATION:  
; APPLICANT: APPLIED RESEARCH SYSTEMS ARS HOLDING N.V.  
; TITLE OF INVENTION: CHEMOKINES MUTANTS IN THE TREATMENT OF MULTIPLE SCLEROSIS  
; FILE REFERENCE: W0465  
; CURRENT APPLICATION NUMBER: US/10/398,457  
; CURRENT FILING DATE: 2003-11-13  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 31  
; LENGTH: 70  
; TYPE: PRT  
; ORGANISM: Escherichia coli  
US-10-398-457-31

Query Match 57.2%; Score 278; DB 6; Length 70;  
Best Local Similarity 68.1%; Pred. No. 8.6e-26;  
Matches 47; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

Qy 24 APMGSDPPTACCFSYTARKLPNFWVDYYETSSLCSPAVVVFQTKRSKQVCADPSESWWQ 83  
Db 1 ASLAADTPTACCFSYTSRQIPQNFADYFETSSQCSKPGVIFLTKRSRQVCADPSEEWVQ 60  
Qy 84 EYVYDLELN 92  
Db 61 KYVSDLELS 69

RESULT 15  
PCT-US03-28745-3  
; Sequence 3, Application PC/TUS0328745  
; GENERAL INFORMATION:  
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.  
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES  
; FILE REFERENCE: 59296.00003  
; CURRENT APPLICATION NUMBER: PCT/US03/28745  
; CURRENT FILING DATE: 2003-09-11  
; NUMBER OF SEQ ID NOS: 1640  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 3  
; LENGTH: 69  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide  
PCT-US03-28745-3

Query Match 56.6%; Score 275; DB 1; Length 69;  
Best Local Similarity 68.7%; Pred. No. 1.9e-25;  
Matches 46; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

Qy 26 MGSDDPPTACCFSYTARKLPNFWVDYYETSSLCSPAVVVFQTKRSKQVCADPSESWWQ 85  
Db 2 LAADTPTACCFSYTSRQIPQNFADYFETSSQCSKPGVIFLTKRSRQVCADPSEEWVQ 61  
Qy 86 VYDLELN 92  
Db 62 VSDLELS 68

Search completed: December 16, 2003, 15:47:23  
Job time : 14.5738 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 16, 2003, 15:39:40 ; Search time 24.6339 Seconds  
(without alignments)  
694.592 Million cell updates/sec

Title: US-09-920-137A-7  
Perfect score: 486  
Sequence: 1 MKLCVTVLSLLMLVAAPFCSP.....VCADPSESWMVQYVYDLELN 92

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 684280 seqs, 185983659 residues

Total number of hits satisfying chosen parameters: 684280

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA: \*  
1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*  
6: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	486	100.0	92	US-08-927-939-20	Sequence 20, Appl
2	486	100.0	92	US-09-834-795A-31	Sequence 31, Appl
3	486	100.0	92	US-09-834-794A-31	Sequence 31, Appl
4	486	100.0	92	US-09-920-137A-7	Sequence 7, Appli
5	486	100.0	92	US-10-137-655-7	Sequence 7, Appli
6	486	100.0	92	US-10-158-366-4	Sequence 4, Appli
7	486	100.0	92	US-10-057-275-7	Sequence 7, Appli
8	486	100.0	92	US-10-293-705-11	Sequence 11, Appl
9	461	94.9	92	US-09-771-023-11	Sequence 11, Appl
10	394	81.1	92	US-10-114-482-3	Sequence 3, Appli
11	375	77.2	69	US-09-792-793A-30	Sequence 30, Appl
12	375	77.2	69	US-10-375-209A-30	Sequence 30, Appl
13	371	76.3	68	US-09-195-457-10	Sequence 10, Appl
14	320	65.8	93	US-08-927-939-49	Sequence 49, Appl
15	320	65.8	93	US-09-151-450-2	Sequence 2, Appli

16	320	65.8	93	9	US-09-834-795A-32	Sequence 32, Appl
17	320	65.8	93	11	US-09-834-794A-32	Sequence 32, Appl
18	320	65.8	93	12	US-10-260-270-3	Sequence 3, Appli
19	320	65.8	93	12	US-10-223-081-330	Sequence 330, App
20	320	65.8	93	12	US-10-223-082-330	Sequence 330, App
21	320	65.8	93	12	US-10-247-671-179	Sequence 179, App
22	320	65.8	93	14	US-10-141-965-6	Sequence 6, Appli
23	320	65.8	93	15	US-10-223-085-330	Sequence 330, App
24	320	65.8	93	15	US-10-223-084-330	Sequence 330, App
25	320	65.8	93	15	US-10-223-088-330	Sequence 330, App
26	320	65.8	93	15	US-10-223-090-330	Sequence 330, App
27	320	65.8	93	15	US-10-223-087-330	Sequence 330, App
28	320	65.8	93	15	US-10-223-083-330	Sequence 330, App
29	320	65.8	93	15	US-10-223-089-330	Sequence 330, App
30	315	64.8	93	12	US-10-301-822-179	Sequence 179, App
31	300.5	61.8	92	8	US-08-927-939-19	Sequence 19, Appl
32	300.5	61.8	92	9	US-09-151-450-3	Sequence 3, Appli
33	300.5	61.8	92	9	US-09-908-599-3	Sequence 3, Appli
34	300.5	61.8	92	9	US-09-334-923A-53	Sequence 53, Appl
35	300.5	61.8	92	9	US-09-834-795A-33	Sequence 33, Appl
36	300.5	61.8	92	9	US-09-334-954A-53	Sequence 53, Appl
37	300.5	61.8	92	9	US-09-908-600-3	Sequence 3, Appli
38	300.5	61.8	92	11	US-09-834-794A-33	Sequence 33, Appl
39	300.5	61.8	92	11	US-09-920-137A-6	Sequence 6, Appli
40	300.5	61.8	92	12	US-10-137-655-6	Sequence 6, Appli
41	300.5	61.8	92	12	US-10-285-572-3	Sequence 3, Appli
42	300.5	61.8	92	12	US-10-165-233A-53	Sequence 53, Appl
43	300.5	61.8	92	12	US-10-116-275-221	Sequence 221, App
44	300.5	61.8	92	14	US-10-158-366-3	Sequence 3, Appli
45	300.5	61.8	92	14	US-10-057-275-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1  
US-08-927-939-20  
; Sequence 20, Application US/08927939  
; Publication No. US20010006640A1  
; GENERAL INFORMATION:  
; APPLICANT: Grainger, David J.  
; APPLICANT: Tatalick, Lauen Marie  
; TITLE OF INVENTION: Compounds and methods to inhibit or  
; TITLE OF INVENTION: augment an inflammatory response.  
; FILE REFERENCE: 295.022US1  
; CURRENT APPLICATION NUMBER: US/08/927,939  
; CURRENT FILING DATE: 1997-09-11  
; NUMBER OF SEQ ID NOS: 83  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 20  
; LENGTH: 92  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-08-927-939-20

Query Match	100.0%;	Score 486;	DB 8;	Length 92;
Best Local Similarity	100.0%;	Pred. No. 6.2e-48;		
Matches	92;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
Qy	1	MKLCVTVLSLLMLVAAPFCSPALSGDPPTACGFSYTARKLPRNFVVDYVETSSLC	60	
Db	1	MKLCVTVLSLLMLVAAPFCSPALSGDPPTACGFSYTARKLPRNFVVDYVETSSLC	60	
Qy	61	PAWVFQTKRSKQVCADPSESWMVQYVYDLELN	92	
Db	61	PAWVFQTKRSKQVCADPSESWMVQYVYDLELN	92	

RESULT 2  
US-09-834-795A-31  
; Sequence 31, Application US/09834795A  
; Patent No. US20020076710A1  
; GENERAL INFORMATION:

APPLICANT: Lawrence, Papsidero  
APPLICANT: Lyn, Dyster  
APPLICANT: Jana, Frustaci  
TITLE OF INVENTION: Detection and Treatment of Breast Cancer  
FILE REFERENCE: 3380/11127-US3  
CURRENT APPLICATION NUMBER: US/09/834,795A  
CURRENT FILING DATE: 2001-04-12  
PRIOR APPLICATION NUMBER: 09/146,580  
PRIOR FILING DATE: 1998-09-03  
PRIOR APPLICATION NUMBER: 60/071,899  
PRIOR FILING DATE: 1998-01-20  
PRIOR APPLICATION NUMBER: 60/092,155  
PRIOR FILING DATE: 1998-07-09  
NUMBER OF SEQ ID NOS: 35  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 31  
LENGTH: 92  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-834-795A-31

Query Match 100.0%; Score 486; DB 9; Length 92;  
Best Local Similarity 100.0%; Pred. No. 6.2e-48;  
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKLCVTVLSLLMLVAAFCSPALSAPMGSDPPTACCFSTARKLPRNFVVDYETSSLCSQ 60  
Db 1 MKLCVTVLSLLMLVAAFCSPALSAPMGSDPPTACCFSTARKLPRNFVVDYETSSLCSQ 60  
QY 61 PAVVFQTKRSKQVCADPSESWSVQYVYDLELN 92  
Db 61 PAVVFQTKRSKQVCADPSESWSVQYVYDLELN 92

RESULT 3  
US-09-834-794A-31  
Sequence 31, Application US/09834794A  
Publication No. US20030026777A1  
GENERAL INFORMATION:  
APPLICANT: Lawrence, Papsidero  
APPLICANT: Lyn, Dyster  
APPLICANT: Jana, Frustaci  
TITLE OF INVENTION: Detection and Treatment of Breast Cancer  
FILE REFERENCE: 3380/11127-US4  
CURRENT APPLICATION NUMBER: US/09/834,794A  
CURRENT FILING DATE: 2001-04-13  
PRIOR APPLICATION NUMBER: 09/146,580  
PRIOR FILING DATE: 1998-09-03  
PRIOR APPLICATION NUMBER: 60/071,899  
PRIOR FILING DATE: 1998-01-20  
PRIOR APPLICATION NUMBER: 60/092,155  
PRIOR FILING DATE: 1998-07-09  
NUMBER OF SEQ ID NOS: 35  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 31  
LENGTH: 92  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-834-794A-31

Query Match 100.0%; Score 486; DB 11; Length 92;  
Best Local Similarity 100.0%; Pred. No. 6.2e-48;  
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKLCVTVLSLLMLVAAFCSPALSAPMGSDPPTACCFSTARKLPRNFVVDYETSSLCSQ 60  
Db 1 MKLCVTVLSLLMLVAAFCSPALSAPMGSDPPTACCFSTARKLPRNFVVDYETSSLCSQ 60  
QY 61 PAVVFQTKRSKQVCADPSESWSVQYVYDLELN 92  
Db 61 PAVVFQTKRSKQVCADPSESWSVQYVYDLELN 92

RESULT 4  
US-09-920-137A-7  
Sequence 7, Application US/09920137A  
Publication No. US20030049725A1  
GENERAL INFORMATION:  
APPLICANT: Coleman, Roger  
APPLICANT: Bandman, Olga  
APPLICANT: Wilde, Craig G.  
TITLE OF INVENTION: NEW CHEMOKINES EXPRESSED IN PANCREAS  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/920,137A  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Luther, Barbara J.  
REGISTRATION NUMBER: 33,954  
REFERENCE/DOCKET NUMBER: PF-0027 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-852-0195  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 92 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: MIP-1b  
US-09-920-137A-7

Query Match 100.0%; Score 486; DB 11; Length 92;  
Best Local Similarity 100.0%; Pred. No. 6.2e-48;  
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKLCVTVLSLLMLVAAFCSPALSAPMGSDPPTACCFSTARKLPRNFVVDYETSSLCSQ 60  
Db 1 MKLCVTVLSLLMLVAAFCSPALSAPMGSDPPTACCFSTARKLPRNFVVDYETSSLCSQ 60  
QY 61 PAVVFQTKRSKQVCADPSESWSVQYVYDLELN 92  
Db 61 PAVVFQTKRSKQVCADPSESWSVQYVYDLELN 92

RESULT 5  
US-10-137-655-7  
Sequence 7, Application US/10137655  
Publication No. US20030138917A1  
GENERAL INFORMATION:  
APPLICANT: Coleman, Roger  
APPLICANT: Bandman, Olga  
APPLICANT: Wilde, Craig G.  
TITLE OF INVENTION: NEW CHEMOKINES EXPRESSED IN PANCREAS  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.

ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/137,655  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Luther, Barbara J.  
REGISTRATION NUMBER: 33,954  
REFERENCE/DOCKET NUMBER: PF-0027 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-852-0195  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 92 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: MIP-1b  
US-10-137-655-7  
Query Match 100.0%; Score 486; DB 12; Length 92;  
Best Local Similarity 100.0%; Pred. No. 6.2e-48;  
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKLCVTVLSLLMLVAFCSPALSGDPPTACCFSTARKLPNFFVVDYETSSLCSQ 60  
Db 1 MKLCVTVLSLLMLVAFCSPALSGDPPTACCFSTARKLPNFFVVDYETSSLCSQ 60  
QY 61 PAVVFQTKRSKQVCADPSESQVQYVYDLELN 92  
Db 61 PAVVFQTKRSKQVCADPSESQVQYVYDLELN 92  
RESULT 6  
US-10-158-366-4  
Sequence 4, Application US/10158366  
Publication No. US20020142398A1  
GENERAL INFORMATION:  
APPLICANT: Coleman, Roger  
Wilde, Craig G.  
Seilhamer, Jeffrey J.  
TITLE OF INVENTION: CHEMOKINE EXPRESSED IN FETAL SPLEEN,  
ITS PRODUCTION AND USES  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/158,366  
FILING DATE: 29-May-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,123B  
FILING DATE: 06-JUN-1995  
APPLICATION NUMBER: US 08/375,346  
FILING DATE: 19-JAN-1995

ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0026-1 DIV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-555-0555  
TELEFAX: 415-845-4166  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 92 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-10-158-366-4  
Query Match 100.0%; Score 486; DB 14; Length 92;  
Best Local Similarity 100.0%; Pred. No. 6.2e-48;  
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKLCVTVLSLLMLVAFCSPALSGDPPTACCFSTARKLPNFFVVDYETSSLCSQ 60  
Db 1 MKLCVTVLSLLMLVAFCSPALSGDPPTACCFSTARKLPNFFVVDYETSSLCSQ 60  
QY 61 PAVVFQTKRSKQVCADPSESQVQYVYDLELN 92  
Db 61 PAVVFQTKRSKQVCADPSESQVQYVYDLELN 92  
RESULT 7  
US-10-057-275-7  
Sequence 7, Application US/10057275  
Publication No. US20020155545A1  
GENERAL INFORMATION:  
APPLICANT: Coleman, Roger  
Bandman, Olga  
Wilde, Craig G.  
TITLE OF INVENTION: NEW CHEMOKINES EXPRESSED IN PANCREAS  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/057,275  
FILING DATE: 25-Jan-2002  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/390,740A  
FILING DATE: February 17, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Luther, Barbara J.  
REGISTRATION NUMBER: 33,954  
REFERENCE/DOCKET NUMBER: PF-0027 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-852-0195  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 92 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:

```
; LIBRARY: GenBank
; CLONE: MIP-1b
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-057-275-7

Query Match      100.0%; Score 486; DB 14; Length 92;
Best Local Similarity 100.0%; Pred. No. 6.2e-48;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLCVTVLSLLMLVAAFCSPPALSAPMGSDPPTACCFSTYARKLPNRFVVDYETSSLC SQ 60
Db 1 MKLCVTVLSLLMLVAAFCSPPALSAPMGSDPPTACCFSTYARKLPNRFVVDYETSSLC SQ 60

QY 61 PAVVFQTKRSKQVCADPSESQVQYVYDLELN 92
Db 61 PAVVFQTKRSKQVCADPSESQVQYVYDLELN 92

RESULT 8
US-10-293-705-11
; Sequence 11, Application US/10293705
; Publication No. US20030083468A1
; GENERAL INFORMATION:
; APPLICANT: Wilde, Craig G.
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Bandman, Olga
; APPLICANT: Seilhamer, Jeffrey J.
; TITLE OF INVENTION: DNA ENCODING LIVER EXPRESSED CHEMOKINE
; FILE REFERENCE: PF-0024-3 CON
; CURRENT APPLICATION NUMBER: US/10/293,705
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: 09/208,803
; PRIOR FILING DATE: 1998-12-09
; PRIOR APPLICATION NUMBER: 08/798,143
; PRIOR FILING DATE: 1997-02-10
; PRIOR APPLICATION NUMBER: 08/347,492
; PRIOR FILING DATE: 1994-11-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PERL Program
; SEQ ID NO 11
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: GenBank ID No. US20030083468A1 g127080
US-10-293-705-11

Query Match      100.0%; Score 486; DB 15; Length 92;
Best Local Similarity 100.0%; Pred. No. 6.2e-48;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLCVTVLSLLMLVAAFCSPPALSAPMGSDPPTACCFSTYARKLPNRFVVDYETSSLC SQ 60
Db 1 MKLCVTVLSLLMLVAAFCSPPALSAPMGSDPPTACCFSTYARKLPNRFVVDYETSSLC SQ 60

QY 61 PAVVFQTKRSKQVCADPSESQVQYVYDLELN 92
Db 61 PAVVFQTKRSKQVCADPSESQVQYVYDLELN 92

RESULT 9
US-09-771-023-11
; Sequence 11, Application US/09771023
; Publication No. US20030027990A1
; GENERAL INFORMATION:
; APPLICANT: Hardiman, Gerard T.
; APPLICANT: Rossi, Devora L.
; APPLICANT: Bacon, Kevin B.
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Schall, Thomas J.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: MAMMALIAN CX3C CHEMOKINE GENES
```

```
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/771,023
; FILING DATE: 2001-01-25
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/786,068
; FILING DATE: 1997-01-21
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/590,828
; FILING DATE: 24-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0569K2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 92 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-771-023-11

Query Match      94.9%; Score 461; DB 11; Length 92;
Best Local Similarity 92.4%; Pred. No. 4.4e-45;
Matches 85; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKLCVTVLSLLMLVAAFCSPPALSAPMGSDPPTACCFSTYARKLPNRFVVDYETSSLC SQ 60
Db 1 MKLCVSALSLLLVAAFCAPGFSAPMGSDPPTSCCFSTYARKLPNRFVVDYETSSLC SQ 60

QY 61 PAVVFQTKRSKQVCADPSESQVQYVYDLELN 92
Db 61 PAVVFQTKRSKQVCADPSESQVQYVYDLELN 92

RESULT 10
US-10-114-482-3
; Sequence 3, Application US/10114482
; Publication No. US20020150992A1
; GENERAL INFORMATION:
; APPLICANT: Wei et al.
; TITLE OF INVENTION: Chemokine Alpha-5
; FILE REFERENCE: PF401D1
; CURRENT APPLICATION NUMBER: US/10/114,482
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: 09/195,106
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 60/066,369
; PRIOR FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; US-10-114-482-3
```



```
Query Match      81.1%; Score 394; DB 14; Length 92;
Best Local Similarity 77.2%; Pred. No. 1.9e-37;
Matches 71; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 1 MKLCVTVLSLLMLVAFCSPALSGPMGSDPPTACCFSTARKLPNRFVVDYYETSSLCQ 60
    |||||: |||: ||||| |||||: |||||: |||||: |||||: |||||: |||||
Db 1 MKLCVSAPFSLLLVAACFDSVLSAPIGSDPPTSCCFSTSRKIHRNFVMDYYETSSLCQ 60
    |||||: |||: ||||| |||||: |||||: |||||: |||||: |||||: |||||

QY 61 PAVVFQTKRSKQVCADPSESWSVQYVYDLELN 92
    ||||| |||: |||: ||||| ||||| ||||| |||||
Db 61 PAVVFLTKGRQICADPSEPVPVNEVYVNDLELN 92

RESULT 11
US-09-792-793A-30
; Sequence 30, Application US/09792793A
; Patent No. US20020168370A1
; GENERAL INFORMATION:
; APPLICANT: McDonald, John R.
; APPLICANT: Coggin, Philip
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
; TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
; FILE REFERENCE: 25020-601D
; CURRENT APPLICATION NUMBER: US/09/792,793A
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 69
; TYPE: PRT
; ORGANISM: homo sapien
; FEATURE:
; OTHER INFORMATION: Human Chemokine Polypeptide: MIP-1-Beta
US-09-792-793A-30

Query Match      77.2%; Score 375; DB 10; Length 69;
Best Local Similarity 100.0%; Pred. No. 2.1e-35;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 APMGSDPPTACCFSTARKLPNRFVVDYYETSSLCQPAVVVFQTKRSKQVCADPSESWSVQ 83
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 APMGSDPPTACCFSTARKLPNRFVVDYYETSSLCQPAVVVFQTKRSKQVCADPSESWSVQ 60

QY 84 EYVYDLELN 92
    ||||| |||||
Db 61 EYVYDLELN 69

RESULT 12
US-10-375-209A-30
; Sequence 30, Application US/10375209A
; Publication No. US20030215421A1
; GENERAL INFORMATION:
; APPLICANT: McDonald, John R.
; APPLICANT: Coggin, Philip
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
; TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
; FILE REFERENCE: 25020-601E
; CURRENT APPLICATION NUMBER: US/10/375,209A
; CURRENT FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 69
; TYPE: PRT
; ORGANISM: homo sapien
; FEATURE:
; OTHER INFORMATION: Human Chemokine Polypeptide: MIP-1-Beta
US-10-375-209A-30

Query Match      77.2%; Score 375; DB 12; Length 69;
Best Local Similarity 100.0%; Pred. No. 2.1e-35;
```

```
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 APMGSDPPTACCFSTARKLPNRFVVDYYETSSLCQPAVVVFQTKRSKQVCADPSESWSVQ 83
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 APMGSDPPTACCFSTARKLPNRFVVDYYETSSLCQPAVVVFQTKRSKQVCADPSESWSVQ 60

QY 84 EYVYDLELN 92
    ||||| |||||
Db 61 EYVYDLELN 69

RESULT 13
US-09-195-457-10
; Sequence 10, Application US/09195457
; Patent No. US20020081623A1
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, TIMOTHY J.
; APPLICANT: JOSE, PETER J.
; APPLICANT: GRIFFITHS-JOHNSON, DAVID A.
; APPLICANT: HSUAN, JOHN J.
; TITLE OF INVENTION: CHEMOTACTIC CYTOKINE
; FILE REFERENCE: 550-33
; CURRENT APPLICATION NUMBER: US/09/195,457
; CURRENT FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/470,323
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: PCT/GB94/02006
; PRIOR FILING DATE: 1994-09-14
; PRIOR APPLICATION NUMBER: GB 9318984.3
; PRIOR FILING DATE: 1993-09-14
; PRIOR APPLICATION NUMBER: GB 94086902.2
; PRIOR FILING DATE: 1994-04-29
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 10
; LENGTH: 68
; TYPE: PRT
; ORGANISM: human
US-09-195-457-10

Query Match      76.3%; Score 371; DB 9; Length 68;
Best Local Similarity 100.0%; Pred. No. 5.8e-35;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 PMGSDPPTACCFSTARKLPNRFVVDYYETSSLCQPAVVVFQTKRSKQVCADPSESWSVQ 84
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 PMGSDPPTACCFSTARKLPNRFVVDYYETSSLCQPAVVVFQTKRSKQVCADPSESWSVQ 60

QY 85 YVYDLELN 92
    ||||| |||||
Db 61 YVYDLELN 68

RESULT 14
US-08-927-939-49
; Sequence 49, Application US/08927939
; Publication No. US20010006640A1
; GENERAL INFORMATION:
; APPLICANT: Grainger, David J.
; APPLICANT: Tatalick, Lauen Marie
; TITLE OF INVENTION: Compounds and methods to inhibit or
; TITLE OF INVENTION: augment an inflammatory response.
; FILE REFERENCE: 295.022US1
; CURRENT APPLICATION NUMBER: US/08/927,939
; CURRENT FILING DATE: 1997-09-11
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 49
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-927-939-49

Query Match      65.8%; Score 320; DB 8; Length 93;
```

Search completed: December 16, 2003, 15:48:24  
Job time : 24.6339 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 16, 2003, 15:36:19 ; Search time 36.6995 Seconds  
(without alignments)  
397.904 Million cell updates/sec

Title: US-09-920-137A-7  
Perfect score: 486  
Sequence: 1 MKLCVTLSLLMLVAFCSP.....VCADPSESQVQYVYDLELN 92

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_19Jun03;\*

1: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:\*

2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*

3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*

4: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:\*

5: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:\*

6: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:\*

7: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:\*

8: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:\*

9: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:\*

10: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:\*

11: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:\*

12: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:\*

13: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:\*

14: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:\*

15: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:\*

16: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:\*

17: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:\*

18: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:\*

19: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:\*

20: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:\*

21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:\*

22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*

23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*

24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	486	100.0	92	11	AA04220
2	486	100.0	92	11	AA05900
3	486	100.0	92	13	AA22712
4	486	100.0	92	16	AA07079
5	486	100.0	92	19	AAW76225
6	486	100.0	92	20	AAW82717
7	486	100.0	92	21	AA15789
8	486	100.0	92	23	AAW52445
9	486	100.0	92	23	AAW52446

10	486	100.0	331	19	AAW76223	Human chemokine MI
11	483	99.4	92	23	ABP65219	Hypoxia-regulated
12	482	99.2	92	23	AAM52447	HIV_Nef1 fusion pr
13	478	98.4	92	24	ABU52388	Human GPCR related
14	476	97.9	92	14	AAR36770	MIP-1beta. Homo s
15	468	96.3	92	23	ABP62996	Human polypeptide
16	465.5	95.8	93	11	AAR05903	pAT 744 gene produ
17	463	95.3	92	24	ABU52387	Human GPCR related
18	457	94.0	92	23	AAM52448	HIV_Nef1 fusion pr
19	455	93.6	92	11	AAR04222	pAT744 gene produc
20	443.5	91.3	87	22	AAU02912	Angiotensin conver
21	441.5	90.8	91	10	AAP91030	Human H400 polypep
22	394	81.1	92	20	AA42166	Rat MIP1-beta prot
23	385	79.2	92	10	AAP93591	Deduced sequence o
24	379	78.0	70	20	AA4226	Chemokine hMCPIb.
25	379	78.0	70	20	AA4227	Chemokine RANTES.
26	379	78.0	73	24	ABU52390	Human GPCR related
27	379	78.0	73	24	ABU52391	Human GPCR related
28	375	77.2	69	21	AA58332	Human macrophage i
29	375	77.2	69	21	AA59040	Amino acid sequenc
30	375	77.2	69	23	AAO21106	MIP-1 beta chemoki
31	375	77.2	69	23	AAO20014	Human chemokine MI
32	375	77.2	69	23	AAO14147	Human MIP-1beta pr
33	375	77.2	73	24	ABU52389	Human GPCR related
34	375	77.2	74	14	AAR38925	ACT-2. Synthetic
35	375	77.2	92	18	AAW01805	Murine macrophage-
36	357	73.5	69	23	AAO21083	Protein of triple
37	320.5	65.9	92	23	AAE22580	Mouse lymphokine m
38	320	65.8	93	12	AAR11553	Human Stem Cell In
39	320	65.8	93	12	AAR14915	LD78beta. Homo sa
40	320	65.8	93	15	AAR62616	Stem cell inhibito
41	320	65.8	93	15	AAR62617	Variant stem cell
42	320	65.8	93	16	AAR70797	MIP-1-alpha. Homo
43	320	65.8	93	20	AAW82721	Human M10 protein
44	320	65.8	93	21	AAW5807	Human chemokine CI
45	320	65.8	93	21	AAW96281	Human chemokine MI

ALIGNMENTS

RESULT 1

AA04220

ID AA04220 standard; protein; 92 AA.

XX

AC AA04220;

XX

DT 25-MAR-2003 (updated)

DT 17-DEC-2001 (updated)

DT 12-SEP-1990 (first entry)

XX

DE Act-2 clone gene product is activated human periferal blood mononuclear cell (PBMC).

DE

XX

KW Periferal blood mononuclear cell; PBMC; lymphokine;

KW cytokine; mitogen; ds.

XX

OS Homo sapiens.

XX

PN USN7312001-N.

XX

PD 13-MAR-1990.

XX

PF 16-DEC-1988; 88US-0312001.

XX

PR 16-DEC-1988; 88US-0312001.

XX

PA (USSH ) US DEPT HEALTH & HUMAN SERVICE.

PA (USDC ) US SEC OF COMMERCE.

XX

PI Siebenlist U, Leonard WJ, Zipfel PJ, Irving SG, Kelly K;

XX

DR WPI; 1990-139708/18.

DR N-PSDB; AAQ03682.

XX New lymphokine-cytokine genes -

PT isolated using mRNA from activated human peripheral blood

PT mononuclear cells and T cells.

XX Disclosure; Page?; 84pp; English.

XX The lymphokine/cytokine-like proteins are associated with the

CC inflammatory response and/or have mitogenic activities. Antigens

CC raised to the proteins may be useful in detection and purification,

CC especially in bioassays of various tumour cells or genetic defects

CC in the inflammatory response.

CC (Note: Revised entry submitted to correct the patent number format of

CC US Government-owned NTIS applications to prevent clashes with ongoing US

CC granted patent numbers. For further information please visit the Derwent

CC web site at [www.derwent.com/dwpi/updates/ntis\\_us.html](http://www.derwent.com/dwpi/updates/ntis_us.html).)

CC (Updated on 25-MAR-2003 to correct PA field.)

XX

SQ Sequence 92 AA;

Query Match 100.0%; Score 486; DB 11; Length 92;

Best Local Similarity 100.0%; Pred. No. 4.4e-49;

Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLCVTVLSLLMLVAFCSPALSPALSGDPPTACCFSTARKLPNRFVVDYETSSLCSQ 60

Db 1 MKLCVTVLSLLMLVAFCSPALSPALSGDPPTACCFSTARKLPNRFVVDYETSSLCSQ 60

QY 61 PAVVFQTKRSKQVCADPSESQVQYVVDLELN 92

Db 61 PAVVFQTKRSKQVCADPSESQVQYVVDLELN 92

RESULT 2

AAR05900

ID AAR05900 standard; protein; 92 AA.

XX

AC AAR05900;

XX

DT 27-NOV-1990 (first entry)

XX

DE Act-2 gene product.

XX

KW Act-2; human lymphokine/cytokine-like protein; mitogenic; ds.

XX Homo sapiens.

XX WO9007009-A.

XX

PD 28-JUN-1990.

XX

PF 15-DEC-1989; 89WO-US05603.

XX

PR 16-DEC-1988; 88US-0285489.

XX

PA (USDC ) US SEC OF COMMERCE.

XX

PI SIEBENLIST U, ZIPFEL PE, KELLEY K, IRVING SG, NAPOLITANO M;

PI LEONARD WJ;

XX

DR WPI; 1990-224535/29.

DR N-PSDB; AAQ05297.

XX

PT New lymphokine-cytokine-like genes - isolated by subtraction

PT cloning and hybridisation using mRNA from activated peripheral

PT blood T cells.

XX

PS Disclosure; Page ?; 137pp; English.

XX

CC Probes raised to the gene product may be used in bioassay of the

CC product, useful in detecting tumour cells, genetic defects in the

CC inflammatory response, or in vivo, for the detection of immune

CC system activation. The proteins may also be used to determine the

CC presence of their receptors.

XX

SQ Sequence 92 AA;

Query Match 100.0%; Score 486; DB 11; Length 92;

Best Local Similarity 100.0%; Pred. No. 4.4e-49;

Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLCVTVLSLLMLVAFCSPALSPALSGDPPTACCFSTARKLPNRFVVDYETSSLCSQ 60

Db 1 MKLCVTVLSLLMLVAFCSPALSPALSGDPPTACCFSTARKLPNRFVVDYETSSLCSQ 60

QY 61 PAVVFQTKRSKQVCADPSESQVQYVVDLELN 92

Db 61 PAVVFQTKRSKQVCADPSESQVQYVVDLELN 92

RESULT 3

AAR22712

ID AAR22712 standard; Protein; 92 AA.

XX

AC AAR22712;

XX

DT 25-MAR-2003 (updated)

DT 22-SEP-1992 (first entry)

XX

DE Human MIP-1 alpha.

XX

KW Macrophage inducible protein; cancer diagnosis; infection;

KW myelopoietic dysfunction; autoimmune disease; ss.

XX

OS Homo sapiens.

XX

PN WO9205198-A.

XX

PD 02-APR-1992.

XX

PF 13-SEP-1991; 91WO-US06489.

XX

PR 14-SEP-1990; 90US-0582636.

XX

PA (CHIR ) CHIRON CORP.

XX

PJ Tekampolso P, Gallegos CA;

XX

XX WPI; 1992-132088/16.

DR N-PSDB; AAQ23729.

XX

PT Expression of pure mammalian macrophage inducible proteins in

PT yeast - to produce MIP for treatment and diagnosis of cancer,

PT infection, myelopoietic dysfunction, etc.

XX

PS Example 3; Fig 1; 38pp; English.

XX

CC This sequence was deduced from the nucleotide sequence AAQ23729.

CC The protein was produced by cloning into the expression vector

CC PYMIP300. The human MIP-lalpha sequence was derived from the

CC lambda gt10 cDNA clone hMIP1-13a, and the GAPDH promoter sequence,

CC alpha factor transcription terminator derived from plasmid pGAL1,

CC the construction of which is described in patent application

CC EP0324-274. Recombinantly produced MIP proteins have diagnostic and

CC therapeutic utility for detecting and treating infections, cancer,

CC myelopoietic dysfunction and autoimmune diseases. Although not

CC directly cytotoxic for WEHI tumour cells, MIP-1 treated macrophages

CC exhibited enhanced antibody-independent macrophage cytotoxicity for

CC tumour targets. MIP-1 treatment stimulated proliferation of mature

CC tissue macrophages; this effect was synergistic with both CSF-1 and

CC GM-CSF. Purified preparations of the recombinantly derived

CC MIP-lalpha peptide alone induced TNF and IL-6 in macrophages, but

CC MIP-lbeta did not. As little as twofold excess MIP-lbeta blocked

CC TNF-induction by MIP-lalpha to a significant degree. Other

CC bioactivity defined for native MIP-1 and recombinant MIP-lalpha





	Matches	92;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0
QY	1	MKLCVTVLSLLMLVA	RCSPAL	SAPMGSDPPTACCF	SYTARKLPRNFVVDYYETSS	CSQ	60			
Db	1	MKLCVTVLSLLMLVA	RCSPAL	SAPMGSDPPTACCF	SYTARKLPRNFVVDYYETSS	CSQ	60			
QY	61	PAWVFQTKRSKQVCAD	PSSESWVQ	EYVYDLELN	92					
Db	61	PAWVFQTKRSKQVCAD	PSSESWVQ	EYVYDLELN	92					
RESULT 6										
AAW82717	ID AAW82717 standard; Protein; 92 AA.									
XX	AC	AAW82717;								
XX	DT	15-MAR-1999 (first entry)								
XX	DE	Human Act-2 protein.								
XX	KW	Chemokine; ZCHEMO-8; human; pathological condition; infection; cancer;								
XX	KW	autoimmune disorder; immunodeficiency; myelopoietic; wound healing;								
XX	KW	transplant; progenitor cell; HIV infection; AIDS; chemotherapy;								
XX	KW	radiation therapy; T cell; macrophage activation inhibitor; B lymphocyte;								
XX	KW	chronic inflammatory disease; infective disease; diagnosis; detection;								
XX	KW	drug screening; gene therapy; Act-2.								
OS	XX	Homo sapiens.								
PN	XX	WO9854326-A1.								
XX	PD	03-DEC-1998.								
XX	PF	19-MAY-1998; 98WO-US10329.								
XX	PR	29-MAY-1997; 97US-0047860.								
XX	PA	(ZYMO ) ZYMOGENETICS INC.								
XX	PI	Sheppard PO;								
XX	DR	WPI; 1999-059841/05.								
XX	PT	New isolated human beta-chemokine, ZCHEMO-8 - used to develop								
XX	PT	products for treating e.g. ischaemia, reperfusion, wound healing,								
XX	PT	autoimmune diseases, inflammation, asthma or infections								
XX	PS	Disclosure; Page 93; 131pp; English.								

```

CC for detection, diagnosis, drug screening or gene therapy.
XX
SQ Sequence 92 AA;

Query Match 100.0%; Score 486; DB 20; Length 92;
Best Local Similarity 100.0%; Pred. No. 4.4e-49;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLCVTVLSLLMLVAAFCSPALSPMGSDPPTACCFSYTARKLPRNFVVDYYETSSLC SQ 60
Db 1 MKLCVTVLSLLMLVAAFCSPALSPMGSDPPTACCFSYTARKLPRNFVVDYYETSSLC SQ 60
QY 61 PAVVFQTKRSKQVCADPSESWSVQYVVDLELN 92
Db 61 PAVVFQTKRSKQVCADPSESWSVQYVVDLELN 92

RESULT 7
AAB15789
ID AAB15789 standard; Protein; 92 AA.
XX
AC AAB15789;
XX
DT 17-JAN-2001 (first entry)
XX
DE Human chemokine MIP1beta SEQ ID NO: 20.
XX
KW Macrophage recruitment; chemokine derivative; MCP-1; osteoporosis;
KW monocyte chemoattractant protein-1; inflammation; atherosclerosis; HIV;
KW AIDS; stroke; psoriasis; autoimmune disease; hypertension; endotoxaemia;
KW basophil-mediated disease; myocardial infarction; acute ischaemia;
KW rheumatoid arthritis; contraception.
XX
OS Homo sapiens.
XX
PN WO200042071-A2.
XX
PD 20-JUL-2000.
XX
PF 12-JAN-2000; 2000WO-US00821.
XX
PR 12-JAN-1999; 99US-0229071.
PR 17-MAR-1999; 99US-0271192.
PR 01-DEC-1999; 99US-0452406.
XX
PA (NEOR-) NEORX CORP.
XX
PI Grainger DJ, Tatalick LM;
XX
DR WPI; 2000-499101/44.
DR N-PSDB; AAA74885.
XX
PT New peptide 3, amide and heterocyclic compounds and saccharide
PT conjugates used for inhibiting chemokine induced activity and for
PT treating e.g. stroke, vascular diseases, autoimmune diseases and tumour
PT growth
XX
PS Example 1; Page 134; 387pp; English.
XX
CC The present invention concerns the identification of a number of
CC chemokines which can be used to produce derivatives, agonists and
CC antagonists which are then useful in disease treatment. The chemokines
CC include sequences AAB15785-B15794, AAB15803-B15813 and AAB15831-B15848.
CC These chemokine derivatives can be used to treat diseases such as
CC autoimmune diseases, atherosclerosis, osteoporosis, HIV infection and
CC AIDS, psoriasis, inflammatory diseases, hypertension, basophil-mediated
CC diseases, endotoxaemia, myocardial infarction, acute ischaemia and
CC rheumatoid arthritis, and can be used to prevent strokes and as
CC contraceptives. The coding sequences for the chemokines can be used in
CC gene therapy for the same diseases, as well as in the production of
CC animal models.
XX
SQ Sequence 92 AA;

```

Query Match 100.0%; Score 486; DB 21; Length 92;  
Best Local Similarity 100.0%; Pred. No. 4.4e-49;  
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLCVTVLSLLMLVAFCSPALSPALSGSDPPTACCFSTYARKLPRNFVVDYETSSLSQ 60  
Db 1 MKLCVTVLSLLMLVAFCSPALSPALSGSDPPTACCFSTYARKLPRNFVVDYETSSLSQ 60

QY 61 PAVVFQTKRSKQVCADPSESWSVQYVVDLELN 92  
Db 61 PAVVFQTKRSKQVCADPSESWSVQYVVDLELN 92

RESULT 8  
AAM52445  
ID AAM52445 standard; Protein; 92 AA.  
XX  
AC AAM52445;  
XX  
DT 03-JUL-2002 (first entry)  
XX  
DE HIV\_Nef1 fusion protein #12.  
XX  
KW Selenoprotein; HIV; Ebola virus; cancer; immune system disorder.  
XX  
OS Homo sapiens.  
XX  
PN US6303295-B1.  
XX  
PD 16-OCT-2001.  
XX  
PF 12-JUL-1996; 96US-0679493.  
XX  
PR 14-JUL-1995; 95US-001203P.  
XX  
PR 01-SEP-1995; 95US-003112P.  
XX  
PA (UYGE-) UNIV GEORGIA RES FOUND INC.  
XX  
PI Taylor EW, Nadimpalli RG, Ramanathan CS;  
XX  
DR WPI; 2002-024734/03.  
XX  
PT New selenoprotein for use in detecting certain viruses, e.g. human  
PT immunodeficiency virus (HIV) or Ebola, cancer and immune system  
PT disorders -  
XX  
PS Disclosure; Columns 73-76; 140pp; English.  
XX  
CC The present invention relates to selenoproteins encoded in the genome of  
CC a virus, where the coding sequence of the selenoprotein is genetically  
CC engineered for expression in a nucleic acid construct. The invention also  
CC discloses a method for identifying selenoprotein coding sequences, for  
CC detecting certain viruses (e.g. HIV or Ebola), cancer and immune system  
CC disorders. The present sequence was used to illustrate the invention.  
XX  
SQ Sequence 92 AA;

Query Match 100.0%; Score 486; DB 23; Length 92;  
Best Local Similarity 100.0%; Pred. No. 4.4e-49;  
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLCVTVLSLLMLVAFCSPALSPALSGSDPPTACCFSTYARKLPRNFVVDYETSSLSQ 60  
Db 1 MKLCVTVLSLLMLVAFCSPALSPALSGSDPPTACCFSTYARKLPRNFVVDYETSSLSQ 60

QY 61 PAVVFQTKRSKQVCADPSESWSVQYVVDLELN 92  
Db 61 PAVVFQTKRSKQVCADPSESWSVQYVVDLELN 92

RESULT 9  
AAM52446

AAM52446 standard; Protein; 92 AA.  
AAM52446;  
03-JUL-2002 (first entry)  
HIV\_Nef1 fusion protein #13.  
Selenoprotein; HIV; Ebola virus; cancer; immune system disorder.  
Homo sapiens.  
US6303295-B1.  
16-OCT-2001.  
12-JUL-1996; 96US-0679493.  
14-JUL-1995; 95US-001203P.  
01-SEP-1995; 95US-003112P.  
(UYGE-) UNIV GEORGIA RES FOUND INC.  
Taylor EW, Nadimpalli RG, Ramanathan CS;  
WPI; 2002-024734/03.  
New selenoprotein for use in detecting certain viruses, e.g. human  
immunodeficiency virus (HIV) or Ebola, cancer and immune system  
disorders -  
Disclosure; Columns 73-76; 140pp; English.  
The present invention relates to selenoproteins encoded in the genome of  
a virus, where the coding sequence of the selenoprotein is genetically  
engineered for expression in a nucleic acid construct. The invention also  
discloses a method for identifying selenoprotein coding sequences, for  
detecting certain viruses (e.g. HIV or Ebola), cancer and immune system  
disorders. The present sequence was used to illustrate the invention.  
Sequence 92 AA;

Query Match 100.0%; Score 486; DB 23; Length 92;  
Best Local Similarity 100.0%; Pred. No. 4.4e-49;  
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLCVTVLSLLMLVAFCSPALSPALSGSDPPTACCFSTYARKLPRNFVVDYETSSLSQ 60  
Db 1 MKLCVTVLSLLMLVAFCSPALSPALSGSDPPTACCFSTYARKLPRNFVVDYETSSLSQ 60

QY 61 PAVVFQTKRSKQVCADPSESWSVQYVVDLELN 92  
Db 61 PAVVFQTKRSKQVCADPSESWSVQYVVDLELN 92

RESULT 10  
AAW76223  
ID AAW76223 standard; Protein; 331 AA.  
XX  
AC AAW76223;  
XX  
DT 02-DEC-1998 (first entry)  
XX  
DE Human chemokine MIP-1beta domain protein from clone MPB-X.  
XX  
KW Chemokine; MIP-1beta; chimeric; human; heterologous protein; inhibitor;  
KW receptor; chemotaxis; migratory cell; angiogenesis; bone; regeneration;  
KW cartilage; ligament; tendon; bone marrow; transplant; inflammation;  
KW autoimmune disorder; vaccine adjuvant; antigen presenting cell; cancer;  
KW HIV; human immunodeficiency virus; therapy; prevention.  
XX  
OS Homo sapiens.  
OS Synthetic.

XX Key Location/Qualifiers  
FH Peptide 1..24  
FT /label= signal  
FT /note= "signal peptide"  
FT Protein 25..331  
FT /label= MIP-1beta  
FT /note= "Chemokine domain"

XX WO9838212-A2.  
XX 03-SEP-1998.  
XX 27-FEB-1998; 98WO-US04002.  
XX 28-FEB-1997; 97US-0808720.

XX (GEMY ) GENETICS INST INC.  
XX Herrmann SH, Swanberg SL;  
XX WPI; 1998-495387/42.  
XX N-PSDB; AAV56825.

XX New chimeric polypeptide(s) - comprise chemokine polypeptide covalently linked to heterologous polypeptide, used for, e.g. chemotactic recruitment of migratory cells  
PS Claim 16c; Page 50-51; 69pp; English.

XX This sequence represents a human chemokine MIP-1beta domain, isolated from cDNA clone MPB-X. This sequence is used in the production of a construct comprising an isolated polynucleotide encoding a chimeric polypeptide which comprises at least 1 chemokine polypeptide covalently attached to at least 1 heterologous polypeptide. By including a heterologous protein in the construction, the chimeric polypeptides will have longer and increased biological activity and can direct the chemokine to a particular site. The chimeric polypeptides can also be designed to inhibit or desensitise chemokine receptors. They can be used to affect the chemotactic recruitment of migratory cells, e.g. for stimulating or inhibiting angiogenesis, for regeneration of bone, cartilage, ligament or tendon, for recruiting transplanted bone marrow cells to bone marrow, or for treating or preventing inflammatory or autoimmune disorders. They can also be used as vaccine adjuvants or to enhance the activity of antigen presenting cells and for treating or preventing HIV infection. Neutralising antibodies binding to the chimeric polypeptide may also be useful therapeutics for both conditions associated with the chemokine corresponding to the chemokine domain of the chimeric polypeptide and also in the treatment of some forms of cancer where abnormal expression of the chemokine is involved.

XX Sequence 331 AA;

Query Match 100.0%; Score 486; DB 19; Length 331;  
Best Local Similarity 100.0%; Pred. No. 2.1e-48;  
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLCVTVLSLLMLVAFCSPALSPMGSDPPTACCFSTARKLPNFFVVDYETSSLSQ 60  
Db 1 MKLCVTVLSLLMLVAFCSPALSPMGSDPPTACCFSTARKLPNFFVVDYETSSLSQ 60  
QY 61 PAVVFQTKRSKQVCADPSESQVQYVYDLELN 92  
Db 61 PAVVFQTKRSKQVCADPSESQVQYVYDLELN 92

RESULT 11  
ABP65219  
ID ABP65219 standard; Protein; 92 AA.  
XX  
AC ABP65219;  
XX  
DT 12-NOV-2002 (first entry)

XX Hypoxia-regulated protein #93.

XX Cytostatic; vasotropic; tranquiliser; antiatherosclerotic; gene therapy;  
KW antiinflammatory; vulnery; gynecological; ophthalmological; vaccine;  
KW hypoxia; tumorigenesis; angiogenesis; apoptosis; cancer;  
KW ischaemic condition; reperfusion injury; retinopathy; neonatal stress;  
KW preeclampsia; atherosclerosis; inflammatory condition; wound healing;  
KW inflammation; erythropoiesis; hair loss; human.

XX Homo sapiens.

XX WO200246465-A2.

XX 13-JUN-2002.

XX 10-DEC-2001; 2001WO-GB05458.

XX 08-DEC-2000; 2000GB-0030076.

XX 08-FEB-2001; 2001GB-0003156.

XX 25-OCT-2001; 2001GB-0025666.

XX (OXFO-) OXFORD BIOMEDICA UK LTD.

XX White J, Mundy CR, Ward NR, Krige D, Kingsman SM, Harris RA;  
PI Rayner WN;

XX WPI; 2002-627238/67.

XX Identifying a gene involved in disease for treating hypoxia-regulated conditions, comprises comparing the transcriptome/proteome of two cell types under different conditions and identifying a differentially regulated gene -

XX Claim 35; Page 401; 538pp; English.

XX The present invention relates to methods for identifying genes and proteins that are implicated in a specific disease or physiological condition. The method comprises comparing the transcriptome/proteome of a specialised cell type implicated in a disease or condition with that of a second specialised cell type, under two experimental conditions, and identifying a gene that is differentially regulated in the two specialised cell types under experimental conditions. ABV7873-ABV78116 and ABP65061-ABP65257 were identified using the methods of the invention. The coding sequences and proteins are useful for treating a disease in a patient, for manufacture of a medicament for treating hypoxia-regulated conditions, and for regulating tumorigenesis, angiogenesis, apoptosis, biological response to hypoxia conditions, or hypoxic-associated pathology in a patient. The coding sequences and proteins are also useful for monitoring the therapeutic treatment of a disease or physiological condition, such as cancer, ischaemic conditions, reperfusion injury, retinopathy, neonatal stress, preeclampsia, atherosclerosis, inflammatory conditions, wound healing, inflammation, erythropoiesis or hair loss.

XX Sequence 92 AA;

Query Match 99.4%; Score 483; DB 23; Length 92;  
Best Local Similarity 98.9%; Pred. No. 9.9e-49;  
Matches 91; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLCVTVLSLLMLVAFCSPALSPMGSDPPTACCFSTARKLPNFFVVDYETSSLSQ 60  
Db 1 MKLCVTVLSLLMLVAFCSPALSPMGSDPPTACCFSTARKLPNFFVVDYETSSLSQ 60  
QY 61 PAVVFQTKRSKQVCADPSESQVQYVYDLELN 92  
Db 61 PAVVFQTKRSKQVCADPSESQVQYVYDLELN 92

RESULT 12  
AAM52447  
ID AAM52447 standard; Protein; 92 AA.  
XX



AC AAM52447;  
XX  
DT 03-JUL-2002 (first entry)  
XX  
DE HIV\_Nef1 fusion protein #14.  
XX  
KW Selenoprotein; HIV; Ebola virus; cancer; immune system disorder.  
XX  
OS Homo sapiens.  
XX  
PN US6303295-B1.  
XX  
PD 16-OCT-2001.  
XX  
PF 12-JUL-1996; 96US-0679493.  
XX  
PR 14-JUL-1995; 95US-001203P.  
PR 01-SEP-1995; 95US-003112P.  
XX  
PA (UYGE-) UNIV GEORGIA RES FOUND INC.  
XX  
PI Taylor EW, Nadimpalli RG, Ramanathan CS;  
XX  
DR WPI; 2002-024734/03.  
XX  
PT New selenoprotein for use in detecting certain viruses, e.g. human  
PT immunodeficiency virus (HIV) or Ebola, cancer and immune system  
PT disorders -  
XX  
PS Disclosure; Columns 73-76; 140pp; English.  
XX  
SQ The present invention relates to selenoproteins encoded in the genome of  
a virus, where the coding sequence of the selenoprotein is genetically  
engineered for expression in a nucleic acid construct. The invention also  
discloses a method for identifying selenoprotein coding sequences, for  
detecting certain viruses (e.g. HIV or Ebola), cancer and immune system  
disorders. The present sequence was used to illustrate the invention.  
XX  
SQ Sequence 92 AA;  
Query Match 99.2%; Score 482; DB 23; Length 92;  
Best Local Similarity 98.9%; Pred. No. 1.3e-48;  
Matches 91; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MKLCVTVLSLLMLVAAFCSAPMSAPMGSDPPTACCFSTARKLPRNFVVDYETSSLSQ 60  
Db 1 MKLCVTVLSLLMLVAAFCSAPMSAPMGSDPPTACCFSTARKLPRNFVVDYETSSLSQ 60  
QY 61 PAVVFQTKRSKQVCADPSESQVYVDLELN 92  
Db 61 PAVVFQTKRGKQVCADPSESQVYVDLELN 92  
RESULT 13  
ABU52388  
ID ABU52388 standard; Protein; 92 AA.  
XX  
AC ABU52388;  
XX  
DT 03-MAR-2003 (first entry)  
XX  
DE Human GPCR related protein NOV36b.  
XX  
KW Human; NOVX; G-protein coupled receptor; GPCR; cancer; cytostatic.  
XX  
OS Homo sapiens.  
XX  
PN WO200279398-A2.  
XX  
PD 10-OCT-2002.  
XX  
PF 08-MAR-2002; 2002WO-US07355.  
XX

PR 08-MAR-2001; 2001US-274194P.  
PR 08-MAR-2001; 2001US-274281P.  
PR 08-MAR-2001; 2001US-274322P.  
PR 09-MAR-2001; 2001US-274849P.  
PR 13-MAR-2001; 2001US-275578P.  
PR 13-MAR-2001; 2001US-275579P.  
PR 13-MAR-2001; 2001US-275601P.  
PR 14-MAR-2001; 2001US-276000P.  
PR 16-MAR-2001; 2001US-276776P.  
PR 19-MAR-2001; 2001US-276994P.  
PR 20-MAR-2001; 2001US-277239P.  
PR 20-MAR-2001; 2001US-277327P.  
PR 20-MAR-2001; 2001US-277338P.  
PR 21-MAR-2001; 2001US-277791P.  
PR 22-MAR-2001; 2001US-277833P.  
PR 23-MAR-2001; 2001US-278152P.  
PR 26-MAR-2001; 2001US-278894P.  
PR 27-MAR-2001; 2001US-278999P.  
PR 27-MAR-2001; 2001US-279036P.  
PR 30-MAR-2001; 2001US-280233P.  
PR 02-APR-2001; 2001US-280802P.  
PR 02-MAY-2001; 2001US-288052P.  
PR 02-MAY-2001; 2001US-288066P.  
PR 02-MAY-2001; 2001US-288228P.  
PR 17-MAY-2001; 2001US-291766P.  
PR 07-JUN-2001; 2001US-296693P.  
PR 08-JUN-2001; 2001US-296856P.  
PR 05-JUL-2001; 2001US-303230P.  
PR 05-JUL-2001; 2001US-303237P.  
PR 08-AUG-2001; 2001US-310913P.  
PR 13-AUG-2001; 2001US-311978P.  
PR 14-AUG-2001; 2001US-312191P.  
PR 16-AUG-2001; 2001US-312916P.  
PR 17-AUG-2001; 2001US-313182P.  
PR 20-AUG-2001; 2001US-313626P.  
PR 21-AUG-2001; 2001US-314018P.  
PR 27-AUG-2001; 2001US-315227P.  
PR 10-SEP-2001; 2001US-318403P.  
PR 10-SEP-2001; 2001US-318510P.  
PR 14-SEP-2001; 2001US-322296P.  
PR 14-SEP-2001; 2001US-322360P.  
PR 27-SEP-2001; 2001US-325378P.  
PR 09-NOV-2001; 2001US-332486P.  
PR 09-NOV-2001; 2001US-345399P.  
PR 07-MAR-2002; 2002US-0094886.  
XX  
XX (CURA-) CURAGEN CORP.  
XX  
PI Kekuda R, Tchernev VT, Liu X, Spytek KA, Patturajan M, Burgess CE;  
PI Vernet CAM, Li L, Gorman L, Malyankar UM, Boldog FL, Guo X;  
PI Shenoy SG, Padigar M, Taupier RJ, Miller CE, Casman SJ, Pena CEA;  
PI Gangolli EA, Gusev V, Smithson G, Zerhusen BD, Gerlach V;  
PI Pochart PF, Fernandes ER, Shimkets RA, Rastelli L, Spaderna SK;  
PI Larochelle WJ, Zhong M, Khramtsov NV, Voss EZ, Herrmann JL;  
XX  
DR WPI; 2003-058423/05.  
DR N-PSDB; ABX70479.  
XX  
PT NOVX polypeptides and polynucleotides, useful for treating a syndrome  
PT related to a human disease associated with the NOVX polypeptide e.g.,  
PT cancer -  
XX  
PS Claim 1; Page 202; 413pp; English.  
XX  
CC The present invention relates to the isolation of novel human  
CC polypeptides referred to as NOVX (NOV1-NOV4), variants of these  
CC proteins, and the polynucleotide sequences encoding them. The NOVX  
CC proteins of the invention are G-protein coupled receptor (GPCR)  
CC related proteins. The sequences of the invention are useful in the  
CC manufacture of a medicament for treating a syndrome related to a  
CC human disease associated with the polypeptides e.g. cancer.  
CC ABU52311-ABU52408 represent the human NOVX proteins of the invention.  
XX

```

Db      61 PAVVFQTKRSKQVCADPSESWMVQYVYDLELN 92

RESULT 15
ABP62996
ID      ABP62996 standard; Protein; 92 AA.
XX
XX      AC      ABP62996;
XX
XX      DT      14-OCT-2002 (first entry)
XX
XX      DE      Human polypeptide SEQ ID NO 433.
XX
XX      KW      Human; vulnery; dermatological; neuroprotective; nootropic; cancer;
XX      KW      antiparkinsonian; immunostimulant; cytostatic; immunosuppressive;
XX      KW      antidiabetic; antiallergic; gene therapy; wound healing; tissue repair;
XX      KW      burn; central nervous system disorder; Alzheimer's disease;
XX      KW      Parkinson's disease; Huntington's disease; immune disorder;
XX      KW      autoimmune disorder; multiple sclerosis; diabetes; allergy.
XX
XX      OS      Homo sapiens.
XX
XX      PN      WO200218424-A2.
XX
XX      PD      07-MAR-2002.
XX
XX      PF      31-AUG-2001; 2001WO-US27093.
XX
XX      PR      01-SEP-2000; 2000US-0654935.
XX
XX      PA      (HYSE-) HYSEQ INC.
XX
XX      PI      Tang YT, Asundi V, Zhou P, Xue AJ, Ren F, Zhang J, Wang J;
XX      PI      Zhao QA, Wang D, Liu C, Drmanac RT, Wehrman T;
XX
XX      DR      WPI; 2002-583321/62.
XX      DR      N-PSDB; ABQ93475.
XX
XX      PT      New polynucleotide and polypeptides, useful for treatment and diagnosis
XX      PT      of Alzheimer's, Parkinson's, Huntington's, amyotrophic lateral
XX      PT      sclerosis, immune deficiencies, cancer, autoimmune disorders, multiple
XX      PT      sclerosis, diabetes and allergies -
XX
XX      PS      Claim 20; SEQ ID NO 433; 284pp + Sequence Listing; English.
XX
XX      CC      The invention relates to an isolated polynucleotide (I) comprising one of
XX      CC      245 sequences (ABQ93288-ABQ93532). Treating a condition comprising
XX      CC      administering to a mammalian subject a composition comprising the protein
XX      CC      (II) encoded by (I) (ABP62809-ABP63053) or an antibody (III) to (II).
XX      CC      (I), (II) and (III) are useful for diagnostic evaluation of disorders.
XX      CC      (I) is useful for gene therapy of diseases and (II) can be used for
XX      CC      therapeutic treatment. Diseases that may be treated include wound healing
XX      CC      and tissue repair, burns, central nervous system disorders (e.g.
XX      CC      Alzheimer's, Parkinson's, Huntington's and amyotrophic lateral
XX      CC      sclerosis), immune deficiencies, cancer, autoimmune disorders, multiple
XX      CC      sclerosis, diabetes and allergies.
XX      CC      Note: The sequence data for this patent did not form part of the printed
XX      CC      specification, but was obtained in electronic format directly from WIPO
XX      CC      at ftp.wipo.int/pub/published_pat_sequences.
XX
XX      SQ      Sequence 92 AA;

Query Match 96.3%; Score 468; DB 23; Length 92;
Best Local Similarity 96.7%; Pred. No. 5.6e-47;
Matches 89; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1 MKLCVTVLSLLMLVAAFCSPALSGSDPPTACCFSTARKLPNFWVDYETSSLSQ 60
Db      1 MKLCVTVLSLLVLVAAFCSLALSGSDPPTACCFSTARKLPNFWVDYETSSLSQ 60
Qy      61 PAVVFQTKRSKQVCADPSESWMVQYVYDLELN 92
Db      61 PAVVFQTKRSKQVCADPSESWMVQYVYDLELN 92

```

Search completed: December 16, 2003, 15:37:48  
Job time : 37.6995 secs

---